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## OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 11:17:50 ; Search time 4940 Seconds  
(without alignments)  
11064.268 Million cell updates/sec

Title: US-10-658-180-246

Perfect score: 1128

Sequence: 1 tcgagagaagagagagctgaa.....tgcttcattagatgag 1128

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBml:.\*  
1: gb ba:.\*  
2: gb \_htg:.\*  
3: gb \_in:.\*  
4: gb \_om:.\*  
5: gb \_ov:.\*  
6: gb \_pat:.\*  
7: gb \_ph:.\*  
8: gb \_pl:.\*  
9: gb \_pr:.\*  
10: gb \_ro:.\*  
11: gb \_sts:.\*  
12: gb \_sy:.\*  
13: gb \_un:.\*  
14: gb \_vi:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1128	100.0	1128	6	AR412266 Sequence
2	1128	100.0	1128	6	AX193968 Sequence
3	1036.2	91.9	1128	6	AR412275 Sequence
4	1036.2	91.9	1128	6	AX193980 Sequence
5	963.4	85.4	1128	6	AR412269 Sequence
6	963.4	85.4	1128	6	AX193972 Sequence
7	909	80.6	1128	6	AR412272 Sequence
8	909	80.6	1128	6	AX193976 Sequence
9	879	77.9	1128	6	AR412278 Sequence
10	879	77.9	1128	6	AX193984 Sequence
11	672.2	59.6	1138	6	AR412253 Sequence
12	672.2	59.6	1138	6	AX193727 Sequence
13	671.4	59.5	1158	6	AR412250 Sequence
14	671.4	59.5	1158	6	AX193723 Sequence
15	671.4	59.5	1161	6	AR412288 Sequence
16	671.4	59.5	1161	6	AX194007 Sequence
17	652.4	57.8	1167	6	AX033231 Solanum c
18	652.4	57.8	1167	6	AR412284 Sequence
19	652.4	57.8	1167	6	AX193992 Sequence

20	619.8	54.9	1390	8	SBUD09331	U09331 Solanum bre
21	618.2	54.8	1437	8	STRNA01	X0125 Potato mRNA
22	616	54.6	1167	6	AR412287	AR412287 Sequence
23	616	54.6	1167	6	AX193996	AX193996 Sequence
24	610.2	54.1	1357	8	STPOTAX	Z27221 S. tuberosum
25	608.4	53.9	1339	6	AR002974	AR002974 S. tuberosum
26	608	53.9	1378	8	STPATB2	AX13178 Potato mRNA
27	608	53.9	1380	6	AR002973	AR002973 Sequence
28	600	53.2	1354	8	STPATB1	X13179 Potato mRNA
29	600	53.2	1404	8	POTPATB1	M21879 Potato patA
30	595	52.7	1405	8	AP498099	AP498099 Solanum c
31	390.6	34.6	1158	6	AR412279	AR412279 Sequence
32	390.6	34.6	1158	6	AX193986	AX193986 Sequence
33	380.2	33.7	1440	8	NTU68484	U68484 Nicotiana t
34	210.2	18.6	1506	6	AX298155	AX298155 Sequence
35	210.2	18.6	1506	8	AP158027	AP158027 Nicotiana
36	198	17.6	5313	8	STPATG	X03932 Solanum tub
37	190	16.8	4029	8	POTPATG	M1880 Potato patA
38	190	16.8	6094	8	STPATG1	X03956 Potato (tet
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42	185.2	16.4	276	6	AR340167	AR340167 Sequence
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44	181.6	16.1	1633	6	AX146911	AX146911 Sequence
45	178.8	15.9	7373	8	STPATP2	X04078 Potato patA

## ALIGNMENTS

RESULT 1	AR412266	Sequence 246 from patent US 6639054.	1128 bp	DNA	linear	PAT 18-DEC-2003
LOCUS	AR412266					
DEFINITION	Sequence 246 from patent US 6639054.					
ACCESSION	AR412266					
VERSION	AR412266.1	GI:40167064				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1128)					
AUTHORS	Alibhai,M.F., Astwood,J.D., McPharrier,C.A. and Sampson,H.A.					
TITLE	Preparation of deaerogenized proteins and permutins					
JOURNAL	Patent: US 6639054-A 246 28-OCT-2003;					
FEATURES	Location/Qualifiers					
source	1..1128					
ORIGIN	/organism="unknown"					
	/mol_type="genomic DNA"					
Query Match	100.0%; Score 1128; DB 6; Length 1128;					
Best Local Similarity	100.0%; Pred. No. 1e-221;					
Matches 1128; Conservative	0; Mismatches 0; Indels 0; Gaps 0;					
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DB	1	TCGAGAAAAGAGGCTGAGCTTCATTTGATTAACAAAATGCTGTGCTCATTAG	60			
QY	61	GCATGCGCACTACTTCAGAGTTTGATTAACATTAACAGCAAGAGGCACTCTGGA	120			
DB	61	GCATGCGCACTACTTCAGAGTTTGATTAACATTAACAGCAAGAGGCACTCTGGA	120			
QY	121	CTGCTGTACATTTGAGATTTGATTAACAGAAATGACTGATGCAAGTTCTTACATGA	180			
DB	121	CTGCTGTACATTTGAGATTTGATTAACAGAAATGACTGATGCAAGTTCTTACATGA	180			
QY	181	CTGATTTTACCTTTTACAGCTTTTCAAGCTCTGATTCAGAAAACAATTAACCTCAGGG	240			
DB	181	CTGATTTTACCTTTTACAGCTTTTCAAGCTCTGATTCAGAAAACAATTAACCTCAGGG	240			
QY	241	TTCAAGAAAATGATTAACAGGCACTACTGAAATGATGATGCTTCTGAGGCTATA	300			

Db	241	TTCAAGAAAATGCAATTAA	CAGGACAACTAC	TGAGAAATGATGATGCTTCTGAGGCTAATA	300	
Qy	301	TGGAATTAATTGTA	CAGTTGCTGAAAACTTA	TGAGAAAGAACCAAGTTTCCGAAACAATC	360	
Db	301	TGGAATTAATTGTA	CAAGTTGGTGTAAAACTTA	TGAGAAAGAACCAAGTTTCCGAAACAATC	360	
Qy	361	CTGAAGACCTATGAGGAACCTCTAA	AGAGTTTGCAAAATTTGCTCTCTGAT	TGAGAAAGAAC	420	
Db	361	CTGAAGACCTATGAGGAACCTCTAA	AGAGTTTGCAAAATTTGCTCTCTGAT	TGAGAAAGAAC	420	
Qy	421	TCCGAGCAAA	CAAAAGCTTCTTA	TGAGCCAGAGCAAGTTGGAGAAATGGTGA	CTGTTCTTA	480
Db	421	TCCGAGCAAA	CAAAAGCTTCTTA	TGAGCCAGAGCAAGTTGGAGAAATGGTGA	CTGTTCTTA	480
Qy	481	GTAATTGATGAGAGTGTGAAATTA	GAGGAGATCAATCCGGCTACATCTCGAATTCGAAATTTCTTGAG	540		
Db	481	GTAATTGATGAGAGTGTGAAATTA	GAGGAGATCAATCCGGCTACATCTCGAATTCGAAATTTCTTGAG	540		
Qy	541	GACAACTTCAGAAATGAGACA	TATATGAGATGCAAGACTTGCGAGATTACTTTGATGTAA	600		
Db	541	GACAACTTCAGAAATGAGACA	TATATGAGATGCAAGACTTGCGAGATTACTTTGATGTAA	600		
Qy	601	TTGAGAGAACAGTACAGAGAGTTTAT	TGACTGCTATGATGATTAAGTACTCAAAATGAAAAACA	660		
Db	601	TTGAGAGAACAGTACAGAGAGTTTAT	TGACTGCTATGATGATTAAGTACTCAAAATGAAAAACA	660		
Qy	661	ATCGAACCTTTGCTGCTGCTCCAA	AGAAATTTGATACCTTTTACTTCGAA	CATAGGACCTCAGA	720	
Db	661	ATCGAACCTTTGCTGCTGCTCCAA	AGAAATTTGATACCTTTTACTTCGAA	CATAGGACCTCAGA	720	
Qy	721	TTTTTAAATCTAGTGTCTCAAA	ATTTTAAAGGCCCAAAATATGATGAGAAATATCTTATGCAAG	780		
Db	721	TTTTTAAATCTAGTGTCTCAAA	ATTTTAAAGGCCCAAAATATGATGAGAAATATCTTATGCAAG	780		
Qy	781	TTCTTCAAGAAAAA	CTTGAGAGAACTGCTGTGCAATCAAGCTTTTGA	CAGAAGTGTCAATC	840	
Db	781	TTCTTCAAGAAAAA	CTTGAGAGAACTGCTGTGCAATCAAGCTTTTGA	CAGAAGTGTCAATC	840	
Qy	841	CNAGCTTTGACATCAAAA	CAAAATAGCCAGTATATTTAC	TAAGTCAATTTTATGCAAACT	900	
Db	841	CNAGCTTTGACATCAAAA	CAAAATAGCCAGTATATTTAC	TAAGTCAATTTTATGCAAACT	900	
Qy	901	CTCCAGAAATTTGAGTGTCTA	AGATGTATGACATTAAGTTATTTCCA	CAGACAGACAGTCTCAACAT	960	
Db	901	CTCCAGAAATTTGAGTGTCTA	AGATGTATGACATTAAGTTATTTCCA	CAGACAGACAGTCTCAACAT	960	
Qy	961	ATTTTCCCTCCGCACTACTTGT	TACTATADACATAGTAATGAGAGATGAATATGAGTTCAATC	1020		
Db	961	ATTTTCCCTCCGCACTACTTGT	TACTATADACATAGTAATGAGAGATGAATATGAGTTCAATC	1020		
Qy	1021	TTGTTGATGATGTCTGTTGCTA	CTGTGTGTCATCCGGCGCTTATTTATCA	CTTACGCTTGCAA	1080	
Db	1021	TTGTTGATGATGTCTGTTGCTA	CTGTGTGTCATCCGGCGCTTATTTATCA	CTTACGCTTGCAA	1080	
Qy	1081	CGAGACTTGACAA	AAAGATCCAGACTTTGCTTCAATTATGATTAAGAG	1128		
Db	1081	CGAGACTTGACAA	AAAGATCCAGACTTTGCTTCAATTATGATTAAGAG	1128		

RESULT 2			
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LOCUS	AXI93968	1128 bp	DNA
DEFINITION	Sequence 246 from Patent WO0149834.		linear
ACCESSION	AXI93968		
VERSION	AXI93968.1	GI:15211580	
KEYWORDS	.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	other sequences; artificial sequences.		
AUTHORS	Alibhai,M.F., Astwood,J.D., Mcwherter,C.A. and Sampson,H.A.		
TITLE	Preparation of deaerigenized proteins and permutins		
JOURNAL	Patent: WO 0149834-A 246 12-JUL-2001;		

FEATURES		MONSANTO COMPANY (US)	
source	Location/Qualifiers		
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	/organism="synthetic construct"		
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Query Match	100.0%;	Score 1128;	DB 6; Length 1128;
Best Local Similarity	100.0%;	Pred. No. 1e-221;	
Matches 1128;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	TCGAGAAAAGAGGGCTTGAAGCTTCATTGAATTACAAAAAATGCTGTGCTCATTAAG	60
DB	1	TCGAGAAAAGAGGGCTTGAAGCTTCATTGAATTACAAAAAATGCTGTGCTCATTAAG	60
QY	61	GCACTGGCACTACTCTTCAGAGTTTGATATAAATATATACAGAAAAGAGCAGCTACCTGA	120
DB	61	GCACTGGCACTACTCTTCAGAGTTTGATATAAATATATACAGAAAAGAGCAGCTACCTGA	120
QY	121	CTGCTGTACATTTGGATGTGTAGTTATACAGAAAATGATCTGATGCGAAGTTCTTACATGA	180
DB	121	CTGCTGTACATTTGGATGTGTAGTTATACAGAAAATGATCTGATGCGAAGTTCTTACATGA	180
QY	181	CTGATTTATACCTTTCTACTGCTTTTCAAGCTCTTGATTCAAAAAACAATTACTCTCAGGG	240
DB	181	CTGATTTATACCTTTCTACTGCTTTTCAAGCTCTTGATTCAAAAAACAATTACTCTCAGGG	240
QY	241	TTCAAGAAAATGCACTTAACAGGCACAATCTACTGAATGATGATGCTTCTGAGGCTAATA	300
DB	241	TTCAAGAAAATGCACTTAACAGGCACAATCTACTGAATGATGATGCTTCTGAGGCTAATA	300
QY	301	TGGAATTAATTAATGATCAAGTTGGTGAATAAATTAATGAAGAAAACAGTTTCGAGAACATC	360
DB	301	TGGAATTAATTAATGATCAAGTTGGTGAATAAATTAATGAAGAAAACAGTTTCGAGAACATC	360
QY	361	CTGAAACCTTATGAGGAAGCTCTTAAGAAGGTTTGCATAATTGCTCTGATAGGAAGAAC	420
DB	361	CTGAAACCTTATGAGGAAGCTCTTAAGAAGGTTTGCATAATTGCTCTGATAGGAAGAAC	420
QY	421	TCCGAGCAAAACAAAGCTTCTTATGAGACCAAGACAGTTGGAGAAAATGCTGCTCTTA	480
DB	421	TCCGAGCAAAACAAAGCTTCTTATGAGACCAAGACAGTTGGAGAAAATGCTGCTCTTA	480
QY	481	GTAATTGATGAGGTGGAAATTAAGAGGATCAATCCGGCTACATCTCGAATTTCTTAAG	540
DB	481	GTAATTGATGAGGTGGAAATTAAGAGGATCAATCCGGCTACATCTCGAATTTCTTAAG	540
QY	541	GACAACTTCAGGAATGAGCAATATATCAGATGCAAACTTGCAGATTACTTTGATGTAA	600
DB	541	GACAACTTCAGGAATGAGCAATATATCAGATGCAAACTTGCAGATTACTTTGATGTAA	600
QY	601	TTGAGAGAACAAAGTACAGAGGTTTATGACTGCTATGATAGTATCTCCAAATGAAAACA	660
DB	601	TTGAGAGAACAAAGTACAGAGGTTTATGACTGCTATGATAGTATCTCCAAATGAAAACA	660
QY	661	ATGCAACCTTTCGTCGTCGCAAAAGAAATGTACTTTTACTTCCTCGAAACATGGCCCTCAGA	720
DB	661	ATGCAACCTTTCGTCGTCGCAAAAGAAATGTACTTTTACTTCCTCGAAACATGGCCCTCAGA	720
QY	721	TTTTTAATCTAGTGTCAAAATTTTAGGCCCAAAATATGATGAGAAAATATCTTATGCAAG	780
DB	721	TTTTTAATCTAGTGTCAAAATTTTAGGCCCAAAATATGATGAGAAAATATCTTATGCAAG	780
QY	781	TTCTTCAAGAAAACTTGAGAAAATCTGTGTGCAATCAAGCTTTGACAGAAAGTTGTCACT	840
DB	781	TTCTTCAAGAAAACTTGAGAAAATCTGTGTGCAATCAAGCTTTGACAGAAAGTTGTCACT	840
QY	841	CAACCTTTCATCAAAAACAAATTAAGCAGTAATATCACTAATGCAAAATTTAGCAACT	900
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LOCUS AR412275  
DEFINITION Sequence 258 from patent US 6639054.  
ACCESSION AR412275  
VERSION AR412275.1 GI:40167073  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1128)  
AUTHORS Alibhai,M.F., Astwood,J.D., McWherter,C.A. and Sampson,H.A.  
TITLE Preparation of deaerogenized proteins and permutins  
JOURNAL Patent: US 6639054-A 258 28-OCT-2003;  
FEATURES  
Source 1..1128  
Location/Qualifiers  
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Query Match 91.9%; Score 1036.2; DB 6; Length 1128;  
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RESULT 4  
AX193980 1128 bp DNA linear PAT 15-AUG-2001  
LOCUS AX193980  
DEFINITION Sequence 258 from Patent WO0149834.  
ACCESSION AX193980  
VERSION AX193980.1 GI:15211589  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Alibhai,M.F., Astwood,J.D., McWherter,C.A. and Sampson,H.A.  
TITLE Preparation of deaerogenized proteins and permutins  
JOURNAL Patent: WO 0149834-A 258 12-JUL-2001;  
MONSANTO COMPANY (US)  
FEATURES  
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Location/Qualifiers  
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Query Match 91.9%; Score 1036.2; DB 6; Length 1128;  
Best Local Similarity 99.2%; Pred. No. 7.8e-203;  
Matches 1041; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
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Db 11 AGAGGCTGAAGCTACATATACAGCAAAAGAGCAGCTACCTGACGTGTCATTTGAT 70  
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QY 137 GTTAGTTATACAGAAAATGACTGATGACAGCAAGTTCTTACATGACTGATTTAATTC 196  
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Db 71 GTTATGTTATACAGAAATGACTGATGACAGAGTTCTTAACATGACTGATTTATACCTTTC 130  
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QY 377 AGCTTAAGAGGTTTGGCAAAATTTGCTCTCTGATAGGAAGAACTCCGAAACAAAGC 436  
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QY 437 TTCTTATGACCGACGACAGTTGGAGAAATGATGATGCTTCTTAATGATGAGAGTGG 496  
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QY 497 AATTAGAGGATATTCGGGCTACCAATTCGAAATTTCTGAAGGACAACTTGAGGAAT 556  
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QY 617 AGAGGTTTATGATGCTGATATGATAGTACTCCAAATGAAACAAATGACCTTTGCTGC 676  
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QY 677 TGGCAAGAATATGATCTTTTACTTGAAACATGGGCTCAGATTTTATCTGATGCTG 736  
Db 611 TGGCAAGAATATGATCTTTTACTTGAAACATGGGCTCAGATTTTATCTGATGCTG 670  
QY 737 TCAATTTTATGGCCCAAAATATGATGAAATATCTTATGCAAGTTCTTCAAGAAACCT 796  
Db 671 TCAATTTTATGGCCCAAAATATGATGAAATATCTTATGCAAGTTCTTCAAGAAACCT 730  
QY 797 TGAAGAAACTCGTGTGATCAAGCTTTGACAGAAATTTGATCAATCAAGCTTTGACATCA 856  
Db 731 TGAAGAAACTCGTGTGATCAAGCTTTGACAGAAATTTGATCAATCAAGCTTTGACATCA 790  
QY 857 AACAAATTAAGCCAGTAAATTTCACTAAGTCAATTTTGAACAACCTCCCAAGTTGATGC 916  
Db 791 AACAAATTAAGCCAGTAAATTTCACTAAGTCAATTTTGAACAACCTCCCAAGTTGATGC 850  
QY 917 TAAGATGATAGATAATGATTAATTCACAGACAGAGCTCAACAAATTTTCTCCGACTTA 976  
Db 851 TAAGATGATAGATAATGATTAATTCACAGACAGAGCTCAACAAATTTTCTCCGACTTA 910  
QY 977 CTCTTGTACTAATATCTAGTAATGAGATGAATATGAGTCAATCTTGTGATGCTGTG 1036  
Db 911 CTCTTGTACTAATATCTAGTAATGAGATGAATATGAGTCAATCTTGTGATGCTGTG 970  
QY 1037 TGTCTACTGTGCTGATCCGGCGGTTATATCAATTAAGCTTGAACGAGCTTGAACAAA 1096  
Db 971 TGTCTACTGTGCTGATCCGGCGGTTATATCAATTAAGCTTGAACGAGCTTGAACAAA 1030  
QY 1097 GGATCCAGACTTTGCTTCAATTAAGTAAAT 1125  
Db 1031 GGATCCAGACTTTGCTTCAATTAAGTAAAT 1059

RESULT 5  
LOCUS AR412269 1128 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 250 from patent US 6639054.  
ACCESSION AR412269

VERSION AR412269.1 GI:40167067  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1128)  
AUTHORS Alibhai, M.F., Astwood, J.D., McWhorter, C.A. and Sampson, H.A.  
TITLE Preparation of deaerogenized proteins and permutans  
JOURNAL Patent: US 6639054-A 250 28-OCT-2003;  
FEATURES  
source 1..1128  
/organism="unknown"  
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Query Match 85.4%; Score 963.4; DB 6; Length 1128;  
Best Local Similarity 99.9%; Pred. No. 7.3e-188;  
Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 24 TCATTGAATTTACAAAAAATGCTGTTGCTCTCATTAAGGCACTGCGACTTCAAGTTT 83  
Db 159 TCATTGAATTTACAAAAAATGCTGTTGCTCTCATTAAGGCACTGCGACTTCAAGTTT 218  
QY 84 GATTAACATATATACAGCAAAAGAGGCACTACCTGGAAGCTGTAATTTATTTATTT 143  
Db 219 GATTAACATATATACAGCAAAAGAGGCACTACCTGGAAGCTGTAATTTATTTATTT 278  
QY 144 ATACAGAAATATGACGATGACAGCAAGTTCTTACATGATGATTAATTTCTTCTACTGCT 203  
Db 279 ATACAGAAATATGACGATGACAGCAAGTTCTTACATGATGATTAATTTCTTCTACTGCT 338  
QY 204 TTTCAAGCTCTTGATTCAAAAAACAATTAACCTGAGGTTTCAAGAAATGATTAACAGGC 263  
Db 339 TTTCAAGCTCTTGATTCAAAAAACAATTAACCTGAGGTTTCAAGAAATGATTAACAGGC 398  
QY 264 ACAACTACTGAATGAGATGATGCTTGAAGGCTTAATATGATTAATTTATTTAGTAACTGGT 323  
Db 399 ACAACTACTGAATGAGATGATGCTTGAAGGCTTAATATGATTAATTTATTTAGTAACTGGT 458  
QY 324 GAAATCTTATGAAAGAAACAGTTTCCGAAACAATCTGAAACCTATGAGAAAGCTCTA 383  
Db 459 GAAATCTTATGAAAGAAACAGTTTCCGAAACAATCTGAAACCTATGAGAAAGCTCTA 518  
QY 384 AAGAGGTTTGAACAATTTGCTCTCTGATAGAGAAACCTCCGACAAACAAGTTCTTAT 443  
Db 519 AAGAGGTTTGAACAATTTGCTCTCTGATAGAGAAACCTCCGACAAACAAGTTCTTAT 578  
QY 444 GACACAGACAGTTGGGAGAAATGATGCTGTTCTTATGATGATGAGAGGTGAATTA 503  
Db 579 GACACAGACAGTTGGGAGAAATGATGCTGTTCTTATGATGATGAGAGGTGAATTA 638  
QY 504 GGGATCATTCGGGCTACCAATTCGAAATTTCTTGAAGCAAACTTCAGAAATGACAAT 563  
Db 639 GGGATCATTCGGGCTACCAATTCGAAATTTCTTGAAGCAAACTTCAGAAATGACAAT 698  
QY 564 AATGCAATGCAAGACTTGCAATTACTTTGATGATTAATGAGAAACAATGACAGAGT 623  
Db 699 AATGCAATGCAAGACTTGCAATTACTTTGATGATTAATGAGAAACAATGACAGAGT 758  
QY 624 TTAATTAATGCTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 683  
Db 759 TTAATTAATGCTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 818  
QY 684 GAAATGTAATTTTACTTTCGAAACATGAGCCCTCAGATTTTATATCTGATGCTCAAT 743  
Db 819 GAAATGTAATTTTACTTTCGAAACATGAGCCCTCAGATTTTATATCTGATGCTCAAT 878  
QY 744 TTAAGCCCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAACTTGAGAA 803  
Db 879 TTAAGCCCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAACTTGAGAA 938  
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Db 999 AAGCAGTAATATTTCACTAAGTCAAAATTTGCAAACTCTCCAGAAATGGATGTAAGATG 1058
Qy 924 TATGACATAAGTTATTTCCAGAGCAGCAGCTCCAAATATTTTCTCCGCAATTAATTTGTT 983
Db 1059 TATGACATAAGTTATTTCCAGAGCAGCAGCTCCAAATATTTTCTCCGCAATTAATTTGTT 1118
Qy 984 ACTPA 988
Db 1119 ACTPA 1123

RESULT 6
AX193972 1128 bp DNA linear PAT 15-AUG-2001
LOCUS Sequence 250 from Patent WO0149834.
DEFINITION AX193972
ACCESSION AX193972
VERSION AX193972.1 GI:15211583
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Alibhai,M.F., Astwood,J.D., McWherter,C.A. and Sampson,H.A.
TITLE Preparation of deaerogenized proteins and permutins
JOURNAL Patent: WO 0149834-A 250 12-JUL-2001;
MONSANTO COMPANY (US)
FEATURES
source
1..1128
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="Synthetic construct"

ORIGIN

Query Match 85.4%; Score 963.4; DB 6; Length 1128;
Best Local Similarity 99.9%; Pred. No. 7.3e-188;
Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 24 TCATTGAATTTACAAAAAATGCTGTTGCTCTCATTTAGGCACTGGCACTTCAAGATT 83
Db 159 TCATTGAATTTACAAAAAATGCTGTTGCTCTCATTTAGGCACTGGCACTTCAAGATT 218
Qy 84 GATPAAAACATATACAGCAAAAGAGGAGCTACCTGGACTGCTGTACATTTGATGTTAGTT 143
Db 219 GATPAAAACATATACAGCAAAAGAGGAGCTACCTGGACTGCTGTACATTTGATGTTAGTT 278
Qy 144 ATACAGAAAATGACTGATGAGCAAGTTCTTACATGACTGATTTACCTTTCTACTGCT 203
Db 279 ATACAGAAAATGACTGATGAGCAAGTTCTTACATGACTGATTTACCTTTCTACTGCT 338
Qy 204 TTTCAAGCTCTTGAATCAAAAAACAATTACCTCAAGGTTCAAGAAAATGCAATTAACAGGC 263
Db 339 TTTCAAGCTCTTGAATCAAAAAACAATTACCTCAAGGTTCAAGAAAATGCAATTAACAGGC 398
Qy 264 ACAACTACTGAAAATGATGATGCTTCTGAGGCTAATATGAAATTTAGTACAAAGTTGCT 323
Db 399 ACAACTACTGAAAATGATGATGCTTCTGAGGCTAATATGAAATTTAGTACAAAGTTGCT 458
Qy 324 GAAAACCTTATTTGAAGAAACAGATTTCGGAAGACAATCTGGAACCTTATGAGAAAGCTCTA 383
Db 459 GAAAACCTTATTTGAAGAAACAGATTTCGGAAGACAATCTGGAACCTTATGAGAAAGCTCTA 518
Qy 384 AAGAGGTTTCAAAATGCTCTCTGATAGGAAAGAACTCCGAGCAAAACAAAGCTTCTTAT 443
Db 519 AAGAGGTTTCAAAATGCTCTCTGATAGGAAAGAACTCCGAGCAAAACAAAGCTTCTTAT 578
Qy 444 GACACGAGACAGTTGGAGAAATGATGACTGTTCTTATGATTTGATGAGAGGTGAATTTAGA 503
Db 579 GACACGAGACAGTTGGAGAAATGATGACTGTTCTTATGATTTGATGAGAGGTGAATTTAGA 638
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Qy 504 GGGATCATTCGGGCTACATTTCTCGAATTTCTTGAAGACAACCTTCAGAAAATGACAAT 563
Db 639 GGGATCATTCGGGCTACATTTCTCGAATTTCTTGAAGACAACCTTCAGAAAATGACAAT 698
Qy 564 AATGACAGTCAAGACTTGCAGATTTACTTGTATGATGTAATGAGAGAACAGTACAGAGGT 623
Db 699 AATGACAGTCAAGACTTGCAGATTTACTTGTATGATGTAATGAGAGAACAGTACAGAGGT 758
Qy 624 TTATGACTGCTATGATGTAATGATCTCCAAATGAAGAAATGACCTTGTGCTGCCAAA 683
Db 759 TTATGACTGCTATGATGTAATGATCTCCAAATGAAGAAATGACCTTGTGCTGCCAAA 818
Qy 684 GAAATGTACTCTTTTACTTCTCGAAGATGGCCCTCAGATTTTAAATCTAGTGTCAATT 743
Db 819 GAAATGTACTCTTTTACTTCTCGAAGATGGCCCTCAGATTTTAAATCTAGTGTCAATT 878
Qy 744 TTAAGCCCAAAATATGATGGAATAATATCTTATGCAAGTTCTTCAAGAAAACCTTGAGAA 803
Db 879 TTAAGCCCAAAATATGATGGAATAATATCTTATGCAAGTTCTTCAAGAAAACCTTGAGAA 938
Qy 804 ACTGCTGTCATCAAGCTTTGACAGAAAGTTGTATCTCAAGCTTTGATCAATCAAAACAAT 863
Db 939 ACTGCTGTCATCAAGCTTTGACAGAAAGTTGTATCTCAAGCTTTGATCAATCAAAACAAT 998
Qy 864 AAGCAGTAATATTTCACTAAGTCAAAATTTAGCAAACTCTCCAGAAATGGATGTAAGATG 923
Db 999 AAGCAGTAATATTTCACTAAGTCAAAATTTAGCAAACTCTCCAGAAATGGATGTAAGATG 1058
Qy 924 TATGACATAAGTTATTTCCAGAGCAGCAGCTCCAAATATTTTCTCCGCAATTAATTTGTT 983
Db 1059 TATGACATAAGTTATTTCCAGAGCAGCAGCTCCAAATATTTTCTCCGCAATTAATTTGTT 1118
Qy 984 ACTPA 988
Db 1119 ACTPA 1123

RESULT 7
AR412272 1128 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 254 from patent US 6639054.
DEFINITION AR412272
ACCESSION AR412272
VERSION AR412272.1 GI:40167070
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1128)
AUTHORS Alibhai,M.F., Astwood,J.D., McWherter,C.A. and Sampson,H.A.
TITLE Preparation of deaerogenized proteins and permutins
JOURNAL Patent: US 6639054-A 254 28-OCT-2003;
FEATURES
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/organism="unknown"
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ORIGIN

Query Match 80.6%; Score 909; DB 6; Length 1128;
Best Local Similarity 100.0%; Pred. No. 1.1e-176;
Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TCATTGAATTTACAAAAAATGCTGTTGCTCTCATTTAGGCACTGGCACTTCAAGATT 83
Db 213 TCATTGAATTTACAAAAAATGCTGTTGCTCTCATTTAGGCACTGGCACTTCAAGATT 272
Qy 84 GATPAAAACATATACAGCAAAAGAGGAGCTACCTGAGCTGCTGATCACTTGAATGTTAGTT 143
Db 273 GATPAAAACATATACAGCAAAAGAGGAGCTACCTGAGCTGCTGATCACTTGAATGTTAGTT 332
Qy 144 ATACAGAAAATGACTGATGAGCAAGTTCTTACATGACTGATTTATTAACCTTTCTACTGCT 203
Db 333 ATACAGAAAATGACTGATGAGCAAGTTCTTACATGACTGATTTATTAACCTTTCTACTGCT 392
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RESULT 9  
AR412278 1128 bp DNA linear PAT 18-DEC-2003  
LOCUS AR412278  
DEFINITION Sequence 262 from patent US 6639054.  
ACCESSION AR412278  
VERSION AR412278.1 GI:40167076  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 1128)  
AUTHORS Alibhai,M.F., Astwood,J.D., McWherter,C.A. and Sampson,H.A.  
TITLE Preparation of deallergenized proteins and permuteins  
JOURNAL Patent: US 6639054-A 262 28-OCT-2003;  
FEATURES  
source location/Qualifiers  
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ORIGIN

Query Match 77.9%; Score 879; DB 6; Length 1128;  
Best Local Similarity 99.4%; Pred. No. 1.6e-170;  
Matches 882; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 239 GGTTCAGAAAATGCACTTAACAGGCACTACTGAAATGATGCTTCTGAGGCTAA 238  
DB 14 GGCTGAAGCTTAAGCTTAACAGGCACTACTGAAATGATGCTTCTGAGGCTAA 73  
QY 299 TATGAATTAATTAATGCAAGTTGGTGAACCTTAATGGAACCAAGTTCCGAGACAA 358  
DB 74 TATGAATTAATTAATGCAAGTTGGTGAACCTTAATGGAACCAAGTTCCGAGACAA 133  
QY 359 TCCTGAACCTTAATGAGAGCTCTAAAGAGTTGGCAAAATGCTCTGATAGGAAGA 418  
DB 134 TCCTGAACCTTAATGAGAGCTCTAAAGAGTTGGCAAAATGCTCTGATAGGAAGA 193  
QY 419 ACTCCGAGCAACAAAGCTCTTAATGAGCAGAGCAGTTGGAGAAATGGGACTGTTCT 478  
DB 194 ACTCCGAGCAACAAAGCTCTTAATGAGCAGAGCAGTTGGAGAAATGGGACTGTTCT 253  
QY 479 TAGTATTAATTAATGCAAGTTGGTGAACCTTAATGGAACCAAGTTCCGAGACAA 538  
DB 254 TAGTATTAATTAATGCAAGTTGGTGAACCTTAATGGAACCAAGTTCCGAGACAA 313  
QY 539 AGGACAACTTCAGAAATGAGCAATATGCAATGCAAGCTTCGAGATTACTTGATGT 598  
DB 314 AGGACAACTTCAGAAATGAGCAATATGCAATGCAAGCTTCGAGATTACTTGATGT 373  
QY 599 AATTGAGAGCAAGTACAGAGGTTTATGACGTCGATATGATGCTCAAAATGAAA 658  
DB 374 AATTGAGAGCAAGTACAGAGGTTTATGACGTCGATATGATGCTCAAAATGAAA 433  
QY 659 CAATGACCTTCGCTGCTGCCAAAGAAATTTGACCTTTTACTTGGAACATGGCCTCA 718  
DB 434 CAATGACCTTCGCTGCTGCCAAAGAAATTTGACCTTTTACTTGGAACATGGCCTCA 493  
QY 719 GATTTTAAATCTAGTGTCAAAATTTAGGCCCAAAATATGATGGAATAATCTTATGCA 778  
DB 494 GATTTTAAATCTAGTGTCAAAATTTAGGCCCAAAATATGATGGAATAATCTTATGCA 553  
QY 779 AGTTCTTCAGAAAATCTTGAGAAAATCTGTCGATCAAGCTTTGACAGAAATTTGAT 838  
DB 554 AGTTCTTCAGAAAATCTTGAGAAAATCTGTCGATCAAGCTTTGACAGAAATTTGAT 613  
QY 839 CTCAGCTTCGATCAAAACAAATAGCAGTAATATTCATGATCAATTTAGCAAA 898  
DB 614 CTCAGCTTCGATCAAAACAAATAGCAGTAATATTCATGATCAATTTAGCAAA 673  
QY 899 CTCCTCAGAAATGAGCTTAAGATGATGACATTAATTTCCACAGACAGCTCCAC 958  
DB 674 CTCCTCAGAAATGAGCTTAAGATGATGACATTAATTTCCACAGACAGCTCCAC 733  
QY 959 ATATTTTCCCTCCGATTAATTTGTTACTAATATGATGAGATGAATATATGATCAA 1018

DB 734 ATATTTTCCCTCCGATTAATTTGTTACTAATATGATGAGATGAATATATGATCAA 793  
QY 1019 TCCTGTGATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1078  
DB 794 TCCTGTGATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 853  
QY 1079 AACGAGCTTCGACAAAGAGATCCAGATTTGCTCAATTAGGTAAT 1125  
DB 854 AACGAGCTTCGACAAAGAGATCCAGATTTGCTCAATTAGGTAAT 900

RESULT 10  
AX193984 1128 bp DNA linear PAT 15-AUG-2001  
LOCUS AX193984  
DEFINITION Sequence 262 from Patent WO0149834.  
ACCESSION AX193984  
VERSION AX193984.1 GI:15211592  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Alibhai,M.F., Astwood,J.D., McWherter,C.A. and Sampson,H.A.  
TITLE Preparation of deallergenized proteins and permuteins  
JOURNAL Patent: WO 0149834-A 262 12-JUL-2001;  
FEATURES  
source location/Qualifiers  
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/note="Synthetic construct"

ORIGIN

Query Match 77.9%; Score 879; DB 6; Length 1128;  
Best Local Similarity 99.4%; Pred. No. 1.6e-170;  
Matches 882; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 239 GGTTCAGAAAATGCACTTAACAGGCACTACTGAAATGATGCTTCTGAGGCTAA 238  
DB 14 GGCTGAAGCTTAATGCACTTAACAGGCACTACTGAAATGATGCTTCTGAGGCTAA 73  
QY 299 TATGAATTAATTAATGCAAGTTGGTGAACCTTAATGGAACCAAGTTCCGAGACAA 358  
DB 74 TATGAATTAATTAATGCAAGTTGGTGAACCTTAATGGAACCAAGTTCCGAGACAA 133  
QY 359 TCCTGAACCTTAATGAGAGCTCTAAAGAGTTGGCAAAATGCTCTGATAGGAAGA 418  
DB 134 TCCTGAACCTTAATGAGAGCTCTAAAGAGTTGGCAAAATGCTCTGATAGGAAGA 193  
QY 419 ACTCCGAGCAACAAAGCTCTTAATGAGCAGAGCAGTTGGAGAAATGGGACTGTTCT 478  
DB 194 ACTCCGAGCAACAAAGCTCTTAATGAGCAGAGCAGTTGGAGAAATGGGACTGTTCT 253  
QY 479 TAGTATTAATTAATGCAAGTTGGTGAACCTTAATGGAACCAAGTTCCGAGACAA 538  
DB 254 TAGTATTAATTAATGCAAGTTGGTGAACCTTAATGGAACCAAGTTCCGAGACAA 313  
QY 539 AGGACAACTTCAGAAATGAGCAATATGCAATGCAAGCTTCGAGATTACTTGATGT 598  
DB 314 AGGACAACTTCAGAAATGAGCAATATGCAATGCAAGCTTCGAGATTACTTGATGT 373  
QY 599 AATTGAGAGCAAGTACAGAGGTTTATGACGTCGATATGATGCTCAAAATGAAA 658  
DB 374 AATTGAGAGCAAGTACAGAGGTTTATGACGTCGATATGATGCTCAAAATGAAA 433  
QY 659 CAATGACCTTCGCTGCTGCCAAAGAAATTTGACCTTTTACTTGGAACATGGCCTCA 718  
DB 434 CAATGACCTTCGCTGCTGCCAAAGAAATTTGACCTTTTACTTGGAACATGGCCTCA 493  
QY 719 GATTTTAAATCTAGTGTCAAAATTTAGGCCCAAAATATGATGGAATAATCTTATGCA 778

Db 494 GATTTTAACTCTAGTGTCAAAATTTTGGCCCAAAATATGATGAAATATCTTATGCA 553  
Qy 779 AGTTCTTCAAGAAAACTTGAGAAAACCTGCTGTCATCAAGCTTTGACAGAGTTGTCA 838  
Db 554 AGTTCTTCAAGAAAACTTGAGAAAACCTGCTGTCATCAAGCTTTGACAGAGTTGTCA 613  
Qy 839 CTCAAGCTTTGACATCAAAACAAATAGCCAGTAAATTTTCACTTAAGTCAAAATTTAGCAA 988  
Db 614 CTCAAGCTTTGACATCAAAACAAATAGCCAGTAAATTTTCACTTAAGTCAAAATTTAGCAA 673  
Qy 899 CTCTCCAGAAATGGATGCTAAGATGATGATCAATGATTTTCCACAGCAGCAGCTCCAC 958  
Db 674 CTCTCCAGAAATGGATGCTAAGATGATGATCAATGATTTTCCACAGCAGCAGCTCCAC 733  
Qy 959 ATAATTTCTCCGCACTTCTTGTATCTAATGATGATGATGATGATGATGATGATGATGAT 1018  
Db 734 ATAATTTCTCCGCACTTCTTGTATCTAATGATGATGATGATGATGATGATGATGATGAT 793  
Qy 1019 TCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1078  
Db 794 TCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 853  
Qy 1079 AACGAGCTTGCACAAAAGGATCCAGCACTTGTCAATGATGATGATGATGATGATGATGAT 1125  
Db 854 AACGAGCTTGCACAAAAGGATCCAGCACTTGTCAATGATGATGATGATGATGATGATGAT 900

## RESULT 11

AR412253 1138 bp DNA linear PAT 18-DEC-2003  
LOCUS AR412253  
DEFINITION Sequence 5 from patent US 6639054.  
ACCESSION AR412253  
VERSION AR412253.1 GI:40167051  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1138)  
AUTHORS Alibhai,M.F., Astwood,J.D., McWhorter,C.A. and Sampson,H.A.  
TITLE Preparation of deaerogenized proteins and permuteneins  
JOURNAL Patent: US 6639054-A 5 28-OCT-2003;  
FEATURES Location/Qualifiers  
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## ORIGIN

Query Match 59.6%; Score 672.2; DB 6; Length 1138;  
Best Local Similarity 99.6%; Pred. No. 5.5e-128;  
Matches 674; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 449 AGGACAGTTGGAGAAATGGTGACTGTTCTTATGATGATGATGATGATGATGATGATGATGAT 508  
Db 25 AGCTCAGTTGGAGAAATGGTGACTGTTCTTATGATGATGATGATGATGATGATGATGATGAT 84  
Qy 509 CATTCCGGCTACCACTTCTGCAATTTCTTGAAGACAATTGAGAAATGACATATATGC 568  
Db 85 CATTCCGGCTACCACTTCTGCAATTTCTTGAAGACAATTGAGAAATGACATATATGC 144  
Qy 569 AGATGCAAGACTTGCAATTTCTTGAATTTGAGAGAACAGTACAGAGTTTAT 628  
Db 145 AGATGCAAGACTTGCAATTTCTTGAATTTGAGAGAACAGTACAGAGTTTAT 204  
Qy 629 GACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 688  
Db 205 GACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 264  
Qy 689 TGATACCTTTTAACTTGAACATGAGCCCTCAGATTTTAACTTGAAGTCAAAATTTTAGG 748  
Db 265 TGATACCTTTTAACTTGAACATGAGCCCTCAGATTTTAACTTGAAGTCAAAATTTTAGG 324  
Qy 749 CCCAAATATGATGAAATATCTTATGCAAGTTCTTCAAGAAAACTTGAGAAACTCG 808

Db 325 CCCAAATATGATGAAATATCTTATGCAAGTTCTTCAAGAAAACTTGAGAAACTCG 384  
Qy 809 TGTGATCAAGCTTTGACAGAAAGTGTCTCATCTCAAGCTTTGACATCAAAACAATATAGCC 868  
Db 385 TGTGATCAAGCTTTGACAGAAAGTGTCTCATCTCAAGCTTTGACATCAAAACAATATAGCC 444  
Qy 869 AGTAAATTTCACTTAAGTCAAAATTTAGCAAACTCCAGAAATGATGATGATGATGATGATGATGAT 928  
Db 445 AGTAAATTTCACTTAAGTCAAAATTTAGCAAACTCCAGAAATGATGATGATGATGATGATGATGAT 504  
Qy 929 CATTAATTTTCCACAGCAGCAGCTCAACATATTTTCTCCGCACTTACTTTGTTACTAA 988  
Db 505 CATTAATTTTCCACAGCAGCAGCTCAACATATTTTCTCCGCACTTACTTTGTTACTAA 564  
Qy 989 TACTAGTAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1048  
Db 565 TACTAGTAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 624  
Qy 1049 TGATCCGGGCTTATTTATCCATTAGCTTGCAACGAGACTTGACACAAAGATTCAGCAATT 1108  
Db 625 TGATCCGGGCTTATTTATCCATTAGCGTTGCAACGAGACTTGACACAAAGATTCAGCAATT 684  
Qy 1109 TGCTTCAATTAGGTAAT 1125  
Db 685 TGCTTCAATTAGGTCAT 701

## RESULT 12

AX193727 1138 bp DNA linear PAT 15-AUG-2001  
LOCUS AX193727  
DEFINITION Sequence 5 from Patent WO0149834.  
ACCESSION AX193727  
VERSION AX193727.1 GI:15211567  
KEYWORDS

SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Alibhai,M.F., Astwood,J.D., McWhorter,C.A. and Sampson,H.A.  
TITLE Preparation of deaerogenized proteins and permuteneins  
JOURNAL Patent: WO 0149834-A 5 12-JUL-2001;  
FEATURES Location/Qualifiers  
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## ORIGIN

Query Match 59.6%; Score 672.2; DB 6; Length 1138;  
Best Local Similarity 99.6%; Pred. No. 5.5e-128;  
Matches 674; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 449 AGGACAGTTGGAGAAATGGTGACTGTTCTTATGATGATGATGATGATGATGATGATGATGAT 508  
Db 25 AGCTCAGTTGGAGAAATGGTGACTGTTCTTATGATGATGATGATGATGATGATGATGATGAT 84  
Qy 509 CATTCCGGCTACCACTTCTGCAATTTCTTGAAGACAATTGAGAAATGACATATATGC 568  
Db 85 CATTCCGGCTACCACTTCTGCAATTTCTTGAAGACAATTGAGAAATGACATATATGC 144  
Qy 569 AGATGCAAGACTTGCAATTTCTTGAATTTGAGAGAACAGTACAGAGTTTAT 628  
Db 145 AGATGCAAGACTTGCAATTTCTTGAATTTGAGAGAACAGTACAGAGTTTAT 204  
Qy 629 GACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 688  
Db 205 GACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 264  
Qy 689 TGATACCTTTTAACTTGAACATGAGCCCTCAGATTTTAACTTGAAGTCAAAATTTTAGG 748  
Db 265 TGATACCTTTTAACTTGAACATGAGCCCTCAGATTTTAACTTGAAGTCAAAATTTTAGG 324



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Db 325 CCCAAATATGATGAAAAATATCTTATGCAAGTTCTTCAAGAAAACTTGAGAACTCG 384  
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QY 809 TGTGATCAAGCTTTGACAGAGTGTGCATCTCAAGTTTGACATCAAAACAAATAAGCC 868  
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|  
|  
Db 385 TGTGATCAAGCTTTGACAGAGTGTGCATCTCAAGTTTGACATCAAAACAAATAAGCC 444  
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|  
QY 869 AGTAATATTCATCAAGTCAAAATTTAGCAAACTCTCCGAATTTGATGCTTAAGATGTGA 928  
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|  
|  
Db 445 AGTAATATTCATCAAGTCAAAATTTAGCAAACTCTCCGAATTTGATGCTTAAGATGTGA 504  
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|  
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QY 929 CATAGATTATTCACAGCAGCAGCTCCAAATATTTTCCCGCATTAATTTGTTACTAA 988  
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|  
|  
Db 505 CATAGATTATTCACAGCAGCAGCTCCAAATATTTTCCCGCATTAATTTGTTACTAA 564  
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QY 989 TACTAGTAATGAGATGAAATATAGATTCATCTGTGTATGATGCTGCTGCTACTGTTGC 1048  
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Db 565 TACTAGTAATGAGATGAAATATAGATTCATCTGTGTATGATGCTGCTGCTACTGTTGC 624  
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QY 1049 TGAATCCGCGCTATTTATTCATTGACCTTGCAAGAGCTTGACAAAGATCCAGATT 1108  
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|  
Db 625 TGAATCCGCGCTATTTATTCATTGACCTTGCAAGAGCTTGACAAAGATCCAGATT 684  
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QY 1109 TGCTCAATTAGGTAAT 1125  
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|  
Db 685 TGCTCAATTAGGTAAT 701  
|  
|  
|

RESULT 13  
AR412250 1158 bp DNA linear PAT 18-DEC-2003  
LOCUS AR412250  
DEFINITION Sequence 1 from patent US 6639054.  
ACCESSION AR412250  
VERSION AR412250.1 GI:40167048  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1158)  
AUTHORS Alibhai,M.F., Astwood,J.D., McWhorter,C.A. and Sampson,H.A.  
TITLE Preparation of deaerogenized proteins and permuteins  
JOURNAL Patent: US 6639054-A 1 28-OCT-2003;  
FEATURES  
source Location/Qualifiers  
1..1158  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Query Match 59.5%; Score 671.4; DB 6; Length 1158;  
Best Local Similarity 99.9%; Pred. No. 8e-128;  
Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 453 CAGTTGGAGAAATGGAATGTAAGTCTGTTCTTATGATGATGAGGTGGAATTAGAGGATCAT 512  
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|  
|  
Db 70 CAGTTGGAGAAATGGAATGTAAGTCTGTTCTTATGATGATGAGGTGGAATTAGAGGATCAT 129  
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|  
|  
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|  
|  
Db 130 CCGGCTACCATTTCTCGAATTTCTTGAAGCAAACTTCAGAAATGGAATTAATGCGAT 189  
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|  
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QY 573 GCAAGCTTGCAATTAATTTGATGTAATGGAAGAAAGTACAGAGGTTTATTTGACT 632  
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|  
|  
Db 190 GCAAGCTTGCAATTAATTTGATGTAATGGAAGAAAGTACAGAGGTTTATTTGACT 249  
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|  
Db 250 GCTATGATTAAGTACTCCAAATGAAACAAATGCACTTTGCTGCTGCAAGAAATTTGTA 309  
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|  
|  
QY 693 CTTTATTTACTTGAACATGCGCCCTCAGATTTTATATCTTAAGTGTCAAAATTTTAGGCCCA 752  
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|  
|  
Db 310 CTTTATTTACTTGAACATGCGCCCTCAGATTTTATATCTTAAGTGTCAAAATTTTAGGCCCA 369  
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QY 753 AAATATGATGAAAAATATCTTATGCAAGTTCTTCAAGAAAACTTGAGAACTCGTGTG 812  
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Db 370 AAATATGATGAAAAATATCTTATGCAAGTTCTTCAAGAAAACTTGAGAACTCGTGTG 429  
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|  
|  
QY 813 CATCAAGCTTTGACAGAGTGTGCATCTCAAGCTTTGACATCAAAACAAATAAGCCAGTA 872  
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Db 430 CATCAAGCTTTGACAGAGTGTGCATCTCAAGCTTTGACATCAAAACAAATAAGCCAGTA 489  
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Db 490 ATATTCATTAAGTCAAAATTTAGCAAACTCTCCGAATTTGATGCTTAAGATGTATGACATA 549  
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QY 933 AGTTATTCACAGCAGCAGCTCCAAATATTTTCTCCGATTAATTTGTTACTAATACT 992  
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Db 550 AGTTATTCACAGCAGCAGCTCCAAATATTTTCTCCGATTAATTTGTTACTAATACT 609  
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QY 993 AGTAATGAGATGAATATGAGTTCATCTGTGTATGATGCTGTGCTACTGTTGCTGAT 1052  
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QY 1053 CCGGCGTTATTTATTCATTAGCTTGCAAGAGCTTGCAACAAAAGATCCAGATTGCT 1112  
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Db 670 CCGGCGTTATTTATTCATTAGCTTGCAAGAGCTTGCAACAAAAGATCCAGATTGCT 729  
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|  
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Db 730 TCAATTAGGTAAT 742  
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|

RESULT 14  
AX193723 1158 bp DNA linear PAT 15-AUG-2001  
LOCUS AX193723  
DEFINITION Sequence 1 from Patent WO0149834.  
ACCESSION AX193723  
VERSION AX193723.1 GI:15211564  
KEYWORDS  
SOURCE Solanum tuberosum (potato)  
ORGANISM Solanum tuberosum  
REFERENCE 1  
AUTHORS Alibhai,M.F., Astwood,J.D., McWhorter,C.A. and Sampson,H.A.  
TITLE Preparation of deaerogenized proteins and permuteins  
JOURNAL Patent: WO 0149834-A 1 12-JUL-2001;  
FEATURES  
source Location/Qualifiers  
1..1158  
/organism="Solanum tuberosum"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:4113"

## ORIGIN

Query Match 59.5%; Score 671.4; DB 6; Length 1158;  
Best Local Similarity 99.9%; Pred. No. 8e-128;  
Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 453 CAGTTGGAGAAATGGAATGTAAGTCTGTTCTTATGATGATGAGGTGGAATTAGAGGATCAT 512  
|  
|  
|  
Db 70 CAGTTGGAGAAATGGAATGTAAGTCTGTTCTTATGATGATGAGGTGGAATTAGAGGATCAT 129  
|  
|  
|  
QY 513 CCGGCTACCATTTCTCGAATTTCTTGAAGCAAACTTCAGAAATGGAATTAATGCGAT 572  
|  
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Db 130 CCGGCTACCATTTCTCGAATTTCTTGAAGCAAACTTCAGAAATGGAATTAATGCGAT 189  
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|  
|  
QY 573 GCAAGCTTGCAATTAATTTGATGTAATGGAAGAAAGTACAGAGGTTTATTTGACT 632  
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|  
|  
Db 190 GCAAGCTTGCAATTAATTTGATGTAATGGAAGAAAGTACAGAGGTTTATTTGACT 249  
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|  
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QY 633 GCTATGATTAAGTACTCCAAATGAAACAAATGCACTTTGCTGCTGCAAGAAATTTGTA 692  
|  
|  
|  
Db 250 GCTATGATTAAGTACTCCAAATGAAACAAATGCACTTTGCTGCTGCAAGAAATTTGTA 309  
|  
|  
|

QY	693	CTTTTACCTCGAACAAGGCCCTCAGATTTTATCCTAGGGTCAATTTTGGCCCA	752
Db	310	CTTTTACTTCGAAACATGGCCCTCAGATTTTATCCTAGGGTCAATTTTGGCCCA	369
QY	753	AAATATGATGGAAAAATATCTTATGCAAGTTCTTCAAGAAAACTTGGAAACTGTGTG	812
Db	370	AAATATGATGAAAAATATCTTATGCAAGTTCTTCAAGAAAACTTGGAAACTGTGTG	429
QY	813	CATCAAGCTTTGACAGAGTTGTATCTCAAGCTTTGATCAACAAACAATTAAGCAGTA	872
Db	430	CATCAAGCTTTGACAGAGTTGTATCTCAAGCTTTGATCAACAAACAATTAAGCAGTA	489
QY	873	ATATTTCACTAAGTCAAATTTAGCAAACCTCTCAGATTTGATGCTAAGATGTATGACATA	932
Db	490	ATATTTCACTAAGTCAAATTTAGCAAACCTCTCAGATTTGATGCTAAGATGTATGACATA	549
QY	933	AGTTATTTCCACAGACAGACGCTCCAAACATATTTTCTCCGACATTACTTTGTTACTAATACT	992
Db	550	AGTTATTTCCACAGACAGACGCTCCAAACATATTTTCTCCGACATTACTTTGTTACTAATACT	609
QY	993	AGTATATGAGATGGAATATAGTTCGAATTTGTGTATGATGCTGTGCTACTGTTGCTAT	1052
Db	610	AGTATATGAGATGGAATATAGTTCGAATTTGTGTATGATGCTGTGCTACTGTTGCTAT	669
QY	1053	CCGGCGTTATTATTCATTAGAGCGTTGCAACGAGACTTGACAAAAGATCCAGACTTTGCT	1112
Db	670	CCGGCGTTATTATTCATTAGAGCGTTGCAACGAGACTTGACAAAAGATCCAGACTTTGCT	729
QY	1113	TCGAATTTAGGTAAAT	1125
Db	730	TCGAATTTAGGTAAAT	742

Oy	693	CTTTTACTCGAAACATGGCCCTCAGATTTTATCTCAGTGGTCAAAATTTTAGCCCA	752
Db	310	CTTTTACTCTGCAACATGGCCCTCAGATTTTATCTCAGTGGTCAAAATTTTAGCCCA	369
Oy	753	AAATATGATGAAATAATCTTATGCAAGTCTTCAGAAAACTTGGAAACTCGTGTG	812
Db	370	AAATATGATGAAATAATCTTATGCAAGTCTTCAGAAAACTTGGAAACTCGTGTG	429
Oy	813	CATAAGCTTTGACAGAAAGTTGTATCTCAAGCTTTCATCAAAACAAATTAAGCCAGTA	872
Db	430	CATCAAGCTTTGACAGAAAGTTGTATCTCAAGCTTTCATCAAAACAAATTAAGCCAGTA	489
Oy	873	ATATTCACTAAGTCMAATTTAGCAAACTCTCCAGATTTGATGCTAAGATGTATGACATA	932
Db	490	ATATTCACTAAGTCMAATTTAGCAAACTCTCCAGATTTGATGCTAAGATGTATGACATA	549
Oy	933	AGTTATTCCACAGACAGACGCTCCAAACATATTTTCTCCGCACTACTTTGTTACTAATATCT	992
Db	550	AGTTATTCCACAGACAGACGCTCCAAACATATTTTCTCCGCACTACTTTGTTACTAATATCT	609
Oy	993	AGTATGAGAGATGAATATGAGTTCAACTCTTGATGATGCTGTGTGCTACTAGTTGCTGAT	1052
Db	610	AGTATGAGAGATGAATATGAGTTCAACTCTTGATGATGCTGTGTGCTACTAGTTGCTGAT	669
Oy	1053	CCGGCGTTATTATTCATTAGAGCTTGCAACGAGACTTGCACAAAAGATCCAGCACTTTCCT	1112
Db	670	CCGGCGTTATTATTCATTAGAGCTTGCAACGAGACTTGCACAAAAGATCCAGCACTTTCCT	729
Oy	1113	TCATTTAGGTTAAT 1125	
Db	730	TCATTTAGGTTAAT 742	

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Job time : 4945 secs

LOCUS	AR412288	1161 bp	DNA	linear	PAT 18-DEC-2003
DEFINITION	Sequence 285 from patent US 6639054.				
ACCESSION	AR412288				
VERSION	AR412288.1	GI:40167086			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
ATTORNS	1 (bases 1 to 1161)				
TITLE	Albhai, M.F., Astwood, J.D., McWhorter, C.A. and Sampson, H.A.				
JOURNAL	Preparation of deaerogenized proteins and permutins				
FEATURES	Patent: US 6639054-A 285-28-OCT-2003;				
source	Location/Qualifiers				
	1..1161				

ORIGIN

Query Match	59.5%	Score 671.4;	DB 6;	Length 1161;
Best Local Similarity	99.9%;	Pred. No. 8e-128;		
Matches 672;	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps	0;

QY	453	CAGTTGGGAGAAATGCTGACTCTTTGATGTTATGATGAGAGGTGGAAATTAGAGGGATCAAT	512
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QY	513	CCGGTACCATTTCTGCAATTTCTTGGAAGACAATTCAGAAATGCAATATGTCAGAT	572
Db	130	CCGGTACCATTTCTGCAATTTCTTGGAAGACAATTCAGAAATGCAATATGTCAGAT	189
QY	573	GCAAGACTTGCAGATTACTTTGATGTAATTGGAGAGACAAGTACAGAGGTTTATTTGACT	632
Db	190	GCAAGACTTGCAGATTACTTTGATGTAATTGGAGAGACAAGTACAGAGGTTTATTTGACT	249
QY	633	GCTATGATTAAGTACCCAAATGAAAACATGACCCCTTGCTGCTGCCAAGAAATTTGTA	692
Db	250	GCTATGATTAAGTACCCAAATGAAAACATGACCCCTTTGCTGCTGCCAAGAAATTTGTA	309

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 11:11:00 ; Search time 660 Seconds  
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Title: US-10-658-180-246

Perfect score: 1128  
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Scoring table: IDENTITY\_NUC  
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Searched: 4390206 seqs, 2959870667 residues

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Minimum DB seq length: 0

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Listing first 45 summaries

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2: geneseqn1980s:\*  
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4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
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12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	1128	100.0	1128	4	AAH73832
2	1128	100.0	1128	12	ADM93059
3	1036.2	91.9	1128	4	AAH73841
4	1036.2	91.9	1128	12	ADM93065
5	963.4	85.4	1128	4	AAH73835
6	963.4	85.4	1128	12	ADM93061
7	909	80.6	1128	4	AAH73838
8	909	80.6	1128	12	ADM93063
9	879	77.9	1128	4	AAH73844
10	879	77.9	1128	12	ADM93067
11	672.2	59.6	1128	4	AAH73819
12	671.4	59.5	1158	4	AAH73816
13	671.4	59.5	1158	12	ADM93077
14	671.4	59.5	1161	4	AAH73854
15	671.4	59.5	1161	12	ADM93076
16	671.4	59.5	1172	2	AAQ72601
17	666.2	59.1	1106	2	AAQ72602
18	652.4	57.8	1167	4	AAH73850
19	652.4	57.8	1167	12	ADM93071
20	618.2	54.8	1106	2	AAQ72610

21	616	54.6	1167	4	AAH73853	AAH73853 Permutectin
22	616	54.6	1167	12	ADM93073	Adm93073 Permutectin
23	613.4	54.4	1172	2	AAQ72608	Aaq72608 Insectici
24	610.8	54.1	1172	2	AAQ72611	Aaq72611 Insectici
25	608.6	54.0	1106	2	AAQ72615	Aaq72615 Insectici
26	608.6	54.0	1106	2	AAQ72612	Aaq72612 Insectici
27	608.4	53.9	1175	2	AAQ72609	Aaq72609 Insectici
28	608.4	53.9	1339	2	AAQ68892	Aaq68892 Patatin c
29	608.4	53.9	1339	2	AAV53682	AAV53682 Nucleotid
30	608	53.9	1171	2	AAQ72606	Aaq72606 Insectici
31	608	53.9	1172	2	AAQ72617	Aaq72617 Insectici
32	608	53.9	1172	2	AAQ72614	AAQ72614 Insectici
33	608	53.9	1380	2	AAQ68891	Aaq68891 Patatin c
34	608	53.9	1380	2	AAV53681	AAV53681 Nucleotid
35	607	53.8	1104	2	AAQ72616	Aaq72616 Insectici
36	607	53.8	1105	2	AAQ72607	Aaq72607 Insectici
37	606.8	53.8	1109	2	AAQ72613	Aaq72613 Insectici
38	594.8	52.7	1172	2	AAQ72620	Aaq72620 Insectici
39	583.6	51.7	1172	2	AAQ72621	Aaq72621 Insectici
40	581.8	51.6	1175	2	AAQ72618	Aaq72618 Insectici
41	380.6	34.6	1158	4	AAH73845	AAH73845 Permutectin
42	380.6	34.6	1158	12	ADM93069	Adm93069 Permutectin
43	390.6	34.6	1164	2	AAQ72603	Aaq72603 Plant ins
44	210.2	18.6	1506	6	ABA01415	ABA01415 Nicotiana
45	185.6	16.5	1509	6	ABA01417	ABA01417 Nicotiana

# ALIGNMENTS

## RESULT 1

AAH73832 standard; DNA, 1128 BP.

AAH73832;

28-SEP-2001 (first entry)

Permutectin protein coding sequence #1.

Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity; larva growth; lipid acyl hydrolase; insecticide; ds.

Unidentified.

WO200149834-A2.

12-JUL-2001.

05-JAN-2001; 2001WO-US000342.

06-JAN-2000; 2000US-0174669P.

(MONS ) MONSANTO CO.

Alibhai MF, Aetwood JD, Mcwherter CA, Sampson HA;

WPI; 2001-441874/47.

Modified potato patatin proteins with reduced antigenicity, useful as insecticides for controlling e.g. round worm and root worm.

Example 7; Page 182-183; 223pp; English.

The present invention relates to modified potato patatins that maintain enzymatic and insecticidal activity but which have reduced allergenicity. Groups (especially Tyr) which bind to anti-patatin antibodies were identified and glycosylation sites involved in antibody binding were removed via site directed mutagenesis. The patatins stunt the growth of larvae so that maturation is prevented or delayed. The patatins also have non-specific lipid acyl hydrolase activity. The modified patatins are also useful for inhibiting the activity of corn round worms. Deallergenic protein can be used as insecticides, as nutritional

CC supplements and as immunising agents. The present sequence was used to  
 CC illustrate the present invention  
 XX  
 SQ Sequence 1128 BP; 372 A; 202 C; 229 G; 325 T; 0 U; 0 Other;

Query Match 100.0%; Score 1128; DB 4; Length 1128;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-291;  
 Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGAGAAAAGAGAGCTGAAGCTTCATTTGAAATTAACAAAAATGCTGTCTCTCATTTAG 60  
 DB 1 TCAGAGAAAAGAGAGCTGAAGCTTCATTTGAAATTAACAAAAATGCTGTCTCTCATTTAG 60  
 QY 61 GCACTGGCACTACTTCAGAGCTTTGATTAACATATACAGCAAAAAGAGGCACTACTGGA 120  
 DB 61 GCACTGGCACTACTTCAGAGCTTTGATTAACATATACAGCAAAAAGAGGCACTACTGGA 120  
 QY 121 CTGCTGTACCTTGGATGCTTGTATATACAGAAAAATGACTGTGACAGCAAGTCTTACATGA 180  
 DB 121 CTGCTGTACCTTGGATGCTTGTATATACAGAAAAATGACTGTGACAGCAAGTCTTACATGA 180  
 QY 181 CTGATTTATTAACCTTTCTACTGCTTTTCAAGCTCTTGATTCAAAAACAATTAACCTCAGG 240  
 DB 181 CTGATTTATTAACCTTTCTACTGCTTTTCAAGCTCTTGATTCAAAAACAATTAACCTCAGG 240  
 QY 241 TTCAGAAAAATGCAATTAACAGGCAACATTAAGTGAATGATGATGCTTCTGAGGCTTAATA 300  
 DB 241 TTCAGAAAAATGCAATTAACAGGCAACATTAAGTGAATGATGATGCTTCTGAGGCTTAATA 300  
 QY 301 TGGAAATTAATAGTACAAAGTGTGTAAGAACTTATTAAGAAACCAAGTTCCGAGAGCAATC 360  
 DB 301 TGGAAATTAATAGTACAAAGTGTGTAAGAACTTATTAAGAAACCAAGTTCCGAGAGCAATC 360  
 QY 361 CTGAAAACCTATGAGAAAGCTCTAAAGAGTTCGAAATTTGCTCTGATAGAGAAAGAAC 420  
 DB 361 CTGAAAACCTATGAGAAAGCTCTAAAGAGTTCGAAATTTGCTCTGATAGAGAAAGAAC 420  
 QY 421 TCCGAGCAAAACAAGCTTTCTTATGACACAGACAGATTGGAGAAATGATGCTGTTCTTA 480  
 DB 421 TCCGAGCAAAACAAGCTTTCTTATGACACAGACAGATTGGAGAAATGATGCTGTTCTTA 480  
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 DB 481 GTATTGATGAGGTGAATTAAGAGGATCAATCCGGTACCACTTCCTGAAATTTCTTGAAG 540  
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 DB 541 GACAACCTTCAGAAATGAGCAATTAATGATGATGATGATGATGATGATGATGATGATGAT 600  
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 DB 601 TTGAGAGAACAGATGACAGAGGTTTATGACCTGCTATGATGATGATGATGATGATGATGAT 660  
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 DB 661 ATGAGACCTTGTGCTGCTGCCAAGAAATTTGACTTTTATCTTGAACATGAGCCCTCAGA 720  
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 DB 721 TTTTAACTCTAGTGTCAATTTTATGAGCCCAAAATATGATGAGAAATATCTTATGCAAG 780  
 QY 781 TTCTTCAAGAAAAAATTGAGAAACTGTGTGATCAAGCTTTGACAGAAAGTGTCACT 840  
 DB 781 TTCTTCAAGAAAAAATTGAGAAACTGTGTGATCAAGCTTTGACAGAAAGTGTCACT 840  
 QY 841 CAAGCTTGTGATCAAAAAGAAATTAAGCAATTAATTAATTAATTAATTAATTAATTAATTA 900  
 DB 841 CAAGCTTGTGATCAAAAAGAAATTAAGCAATTAATTAATTAATTAATTAATTAATTAATTA 900  
 QY 901 CTCAGAAATGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
 DB 901 CTCAGAAATGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960

QY 961 ATTTTCTCCGCACTTACTTTGTTACTTAATTAAGTAATGAGATGATGATGATGATGATGAT 1020  
 DB 961 ATTTTCTCCGCACTTACTTTGTTACTTAATTAAGTAATGAGATGATGATGATGATGATGAT 1020  
 QY 1021 TTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
 DB 1021 TTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
 QY 1081 CGAGACTTGCACAAAAGATTCAGCAATTTGCTTCAATTAAGTAAATGAG 1128  
 DB 1081 CGAGACTTGCACAAAAGATTCAGCAATTTGCTTCAATTAAGTAAATGAG 1128

## RESULT 2

ADM93059  
 ID ADM93059 standard; DNA; 1128 BP.  
 XX  
 AC ADM93059;  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Permutated plasmid DNA #1.  
 XX  
 KW lipid acyl hydrolase; corn rootworm; insect infestation; plant;  
 KW insect control; nutritional supplement; ds; permutated.  
 XX  
 OS Synthetic.  
 XX  
 PN US6657046-B1.  
 XX  
 PD 02-DEC-2003.  
 XX  
 PF 05-JAN-2001; 2001US-00755274.  
 XX  
 PR 06-JUN-2000; 2000US-0174669P.  
 PR 21-JUL-2000; 2000US-0219912P.  
 XX  
 PA (MONS) MONSANTO TECHNOLOGY LLC.  
 XX  
 PI Alibhai MF, Rydel TJ;  
 XX  
 DR WPI; 2004-058368/06.  
 DR P-PSDB; ADM93060.  
 XX  
 XX  
 PT New lipid acyl hydrolase proteins, useful for inhibiting insect  
 PT infestation of a plant or plant part, for controlling insects, as  
 PT nutritional supplements, or in immunotherapy protocols.  
 XX  
 PS Example 6; SEQ ID NO 20; 73pp; English.  
 XX  
 CC The invention relates to an isolated peptide exhibiting lipid acyl  
 CC hydrolase activity and corn rootworm insect inhibitory bioactivity. The  
 CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation  
 CC of a plant or plant part, for controlling insects (e.g. corn rootworm),  
 CC as nutritional supplements, and in immunotherapy protocols. The present  
 CC sequence represents permutated plasmid DNA.  
 XX  
 SQ Sequence 1128 BP; 372 A; 202 C; 229 G; 325 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1128; DB 12; Length 1128;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-291;  
 Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCAGAGAAAAGAGAGCTGAAGCTTCATTTGAAATTAACAAAAATGCTGTCTCTCATTTAG 60  
 DB 1 TCAGAGAAAAGAGAGCTGAAGCTTCATTTGAAATTAACAAAAATGCTGTCTCTCATTTAG 60  
 QY 61 GCACTGGCACTACTTCAGAGCTTTGATTAACATATACAGCAAAAAGAGGCACTACTGGA 120  
 DB 61 GCACTGGCACTACTTCAGAGCTTTGATTAACATATACAGCAAAAAGAGGCACTACTGGA 120  
 QY 121 CTGCTGTACCTTGGATGCTTGTATATACAGAAAAATGACTGTGACAGCAAGTCTTACATGA 180  
 DB 121 CTGCTGTACCTTGGATGCTTGTATATACAGAAAAATGACTGTGACAGCAAGTCTTACATGA 180

Db	121	CTGCTGTACATTTGGATGTGTAACTTATACGAAATAATGACGTAGCAGCAAGTCTTAACATGA	180
Qy	181	CTGATTAATTAACCTTTCTTAACCTCTTTTCAAGCTCTTGATTTCAAAAAACATTAACCTCAGGG	240
Db	181	CTGATTAATTAACCTTTCTTAACCTCTTTTCAAGCTCTTGATTTCAAAAAACATTAACCTCAGGG	240
Qy	241	TTTCAAGAAAAATGCAATTTAAACAGGCAACACTACTGAAATGGAATGATGCTTCAGAGCTAATA	300
Db	241	TTTCAAGAAAAATGCAATTTAAACAGGCAACACTACTGAAATGGAATGATGCTTCAGAGCTAATA	300
Qy	301	TGGAATTAATTAATGTACAAGTTGATGATGAAAATTATGGAAGAAACCAAGTTCCGAAAGCAATC	360
Db	301	TGGAATTAATTAATGTACAAGTTGATGATGAAAATTATGGAAGAAACCAAGTTCCGAAAGCAATC	360
Qy	361	CTGAAACCTTAATGAGAAAGCTCTAAAGAGTTTGCAAAATTCCTCTGTGATAGAAAGAAC	420
Db	361	CTGAAACCTTAATGAGAAAGCTCTAAAGAGTTTGCAAAATTCCTCTGTGATAGAAAGAAC	420
Qy	421	TCCAGACAAACAAAGCTTTCTTAATGACACAGACACAGTTGGGGAATATGATGACTGTTCTTA	480
Db	421	TCCAGACAAACAAAGCTTTCTTAATGACACAGACACAGTTGGGGAATATGATGACTGTTCTTA	480
Qy	481	GTAATTGATGAGAGTGGAATTTAGAGGAAATCAATCCGGGCTACCAATCTCGAATTTCTTGAG	540
Db	481	GTAATTGATGAGAGTGGAATTTAGAGGAAATCAATCCGGGCTACCAATCTCGAATTTCTTGAG	540
Qy	541	GACAACTTCAGGAATATGACATATAATGACAGATGCAAGACTTCGAGATTAACCTTTGATGTA	600
Db	541	GACAACTTCAGGAATATGACATATAATGACAGATGCAAGACTTCGAGATTAACCTTTGATGTA	600
Qy	601	TTGAGAGAAACAAGTACAGAGAGTTTATTTAGCTGTATGATAGTAATCTCAAAATGAAAACA	660
Db	601	TTGAGAGAAACAAGTACAGAGAGTTTATTTAGCTGTATGATAGTAATCTCAAAATGAAAACA	660
Qy	661	ATGCAACCTTGTCTGTCCGCAAAAGAAATGTAACCTTTTACTTGGAATAGAGCCCTCAGA	720
Db	661	ATGCAACCTTGTCTGTCCGCAAAAGAAATGTAACCTTTTACTTGGAATAGAGCCCTCAGA	720
Qy	721	TTTTTAATCCTAGTGTCAAAATTTTATGAGCCCAAAATATGATGAAATATCTTAATGCAAG	780
Db	721	TTTTTAATCCTAGTGTGTCAAAATTTTATGAGCCCAAAATATGATGAAATATCTTAATGCAAG	780
Qy	781	TTCTTCAAGAAAACTTGGAGAAACTCGTGTGCATCAAGCTTTGACAGAAATTTGTATCT	840
Db	781	TTCTTCAAGAAAACTTGGAGAAACTCGTGTGCATCAAGCTTTGACAGAAATTTGTATCT	840
Qy	841	CAAGCTTTGACATCAAAACAATAAGCAGTAATTAATCACTAATGCAAAATTTAGCAAACT	900
Db	841	CAAGCTTTGACATCAAAACAATAAGCAGTAATTAATCACTAATGCAAAATTTAGCAAACT	900
Qy	901	CTCAGAAATGGAATGCTAAGATGTAATGACATTAAGTATTTCCACAGCAGCAGCTCCAAAT	960
Db	901	CTCAGAAATGGAATGCTAAGATGTAATGACATTAAGTATTTCCACAGCAGCAGCTCCAAAT	960
Qy	961	ATTTTCCCTCCGCAATTAATCTTTGTACTAATACTAATGAAATGGAATATGATGATTCATC	1020
Db	961	ATTTTCCCTCCGCAATTAATCTTTGTACTAATACTAATGAAATGGAATATGATGATTCATC	1020
Qy	1021	TTGTTGATGATGCTGTGTTGCTAATGTTGCTGATCCGGCGTTATTTATCCATTTAGCGTTGCAA	1080
Db	1021	TTGTTGATGATGCTGTGTTGCTAATGTTGCTGATCCGGCGTTATTTATCCATTTAGCGTTGCAA	1080
Qy	1081	CGAAGCTTGACAAAGAGATCCAGACTTTGCTTCAATTAAGTAATGAG	1128
Db	1081	CGAAGCTTGACAAAGAGATCCAGACTTTGCTTCAATTAAGTAATGAG	1128
RESULT 3			
AAH73841			
ID AAH73841 standard; DNA; 1128 BP.			
XX AAH73841;			
XX			

DT	28-SEP-2001	(first entry)
XX	Permuterin protein coding sequence #4.	
XX	Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;	
XX	larva growth; lipid acyl hydrolase; insecticide; ds.	
XX	Unidentified.	
OS	Unidentified.	
PN	MO200149834-A2.	
XX	12-JUL-2001.	
PD	05-JAN-2001; 2001WO-US000342.	
PF	06-JAN-2000; 2000US-0174669P.	
XX	(MONS ) MONSANTO CO.	
PA	Albhai ME, Astwood JD, Mcwherter CA, Sampson HA;	
PI	WPI; 2001-441874/47.	
DR	Modified potato patatin proteins with reduced antigenicity, useful as	
XX	insecticides for controlling e.g. round worm and root worm.	
PT	Example 10; Page 190; 223pp; English.	
XX	The present invention relates to modified potato patatins that maintain	
XX	enzymatic and insecticidal activity but which have reduced allergenicity.	
CC	Groups (especially Tyr) which bind to anti-patatin antibodies were	
CC	identified and glycosylation sites involved in antibody binding were	
CC	removed via site directed mutagenesis. The patatins stunt the growth of	
CC	larvae so that maturation is prevented or delayed. The patatins also have	
CC	non-specific lipid acyl hydrolase activity. The modified patatins are	
CC	also useful for inhibiting the activity of corn round worms.	
CC	Dealergenised protein can be used as insecticides, as nutritional	
CC	supplements and as immunising agents. The present sequence was used to	
CC	illustrate the present invention	
XX	Sequence 1128 BP; 372 A; 202 C; 228 G; 326 T; 0 U; 0 Other;	
XX	Query Match 91.9%; Score 1036.2; DB 4; Length 1128;	
XX	Best Local Similarity 99.2%; Pred. No. 9.9e-267;	
XX	Matches 1041; Conservative 0; Mismatches 8; Indels 0; Gaps 0;	
QY	77 AGAGTTGATATAAAACATTAACAGCAAAAGAGCGAGCTACCGAGCTGCTGATACATTTGGAT	136
DB	11 AGAGCGCTGAACCTCATATATACAGCAAAAGAGCGAGCTACCGAGCTGCTGATACATTTGGAT	70
QY	137 GTTAGTTATACAGAAATATGACTGATGCGAGCAAGTTCTTACATGACTGTTATACCTTTC	196
DB	71 GTTAGTTATACAGAAATATGACTGATGCGAGCAAGTTCTTACATGACTGTTATACCTTTC	130
QY	197 TACTGCTTTTCAAGCTCTTGATTCAAAAAACAATTAACCTCAGGGTTCAAGAAAAATGCATT	256
DB	131 TACTGCTTTTCAAGCTCTTGATTCAAAAAACAATTAACCTCAGGGTTCAAGAAAAATGCATT	190
QY	257 AACAGGCAACATCTACTGAAATGATGATGCTTCTGAGGCTAATATGAAATTTATAGTACA	316
DB	191 AACAGGCAACATCTACTGAAATGATGATGCTTCTGAGGCTAATATGAAATTTATAGTACA	250
QY	317 AGTTGGTGAATCTTATGAGAAACAGGTTCCGAGAGCAATCCGTAAGAGG	376
DB	251 AGTTGGTGAATCTTATGAGAAACAGGTTCCGAGAGCAATCCGTAAGAGG	310
QY	377 AGCTTAAAGAGGTTTGCAAAATTTCTCTGATAGAGAAAGAACTCCGAGCAACAAAGC	436
DB	311 AGCTTAAAGAGGTTTGCAAAATTTCTCTGATAGAGAAAGAACTCCGATCAACAAAGC	370
QY	437 TTCTTATAGACACGAGGTTGGAGAAATGATGATCTTTATAGTATTTAGAGAGG	496
DB	371 TTCTTATAGACACGAGGTTGGAGAAATGATGATCTTTATAGTATTTAGAGAGG	430

QY 497 AATTAGAGGATTCCTGGCTACCAATTCGAAATTTCTTGAAGACCACTTCAGAAAT 556  
 DB 431 AATTAGAGGATTCCTGGCTACCAATTCGAAATTTCTTGAAGACCACTTCAGAAAT 490  
 QY 557 GGCAATTAATGACGATGACGATGACGATGACGATGACGATGACGATGACGATGAC 616  
 DB 491 GGCAATTAATGACGATGACGATGACGATGACGATGACGATGACGATGACGATGAC 550  
 QY 617 AGGAGGTTTATGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 676  
 DB 551 AGGAGGTTTATGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 610  
 QY 677 TGGCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 736  
 DB 611 TGGCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 670  
 QY 737 TCAAAATTTTGGCCCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 796  
 DB 671 TCAAAATTTTGGCCCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 730  
 QY 797 TGGAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 856  
 DB 731 TGGAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 790  
 QY 857 AACCAATTAAGCCAGTAATATATCACTAAGTCAAAATTTAGCAAACTCTCCAGAAATTTGATGC 916  
 DB 791 AACCAATTAAGCCAGTAATATATCACTAAGTCAAAATTTAGCAAACTCTCCAGAAATTTGATGC 850  
 QY 917 TAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 976  
 DB 851 TAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 910  
 QY 977 CTCTGTTACTAATATAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1036  
 DB 911 CTCTGTTACTAATATAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 970  
 QY 1037 TGGTACTGTTGCTGATGCTGGCGTTATATTCATTAAGCTTGCAACGAGCTTGCAAAA 1096  
 DB 971 TGGTACTGTTGCTGATGCTGGCGTTATATTCATTAAGCTTGCAACGAGCTTGCAAAA 1030  
 QY 1097 GGATCCAGCATTTGCTTCAATTAAGTAT 1125  
 DB 1031 GGATCCAGCATTTGCTTCAATTAAGTAT 1059

RESULT 4

ADM93065 standard; DNA; 1128 BP.  
 ID ADM93065;  
 AC ADM93065;  
 XX 03-JUN-2004 (first entry)  
 DT 03-JUN-2004 (first entry)  
 XX Permutatein plasmid DNA #4.  
 DE Permutatein plasmid DNA #4.  
 XX lipid acyl hydrolase; corn rootworm; insect infestation; plant;  
 KM insect control; nutritional supplement; ds; permutatein.  
 XX Synthetic.  
 OS Synthetic.  
 XX US6657046-B1.  
 PN US6657046-B1.  
 PD 02-DEC-2003.  
 XX 02-DEC-2003.  
 PF 05-JAN-2001; 2001US-00755274.  
 XX 05-JAN-2001; 2001US-00755274.  
 XX 06-JAN-2000; 2000US-0174669P.  
 PR 21-JUL-2000; 2000US-0219912P.  
 XX 21-JUL-2000; 2000US-0219912P.  
 PA (MONS ) MONSANTO TECHNOLOGY LLC.  
 XX (MONS ) MONSANTO TECHNOLOGY LLC.  
 PI Alibhai MF, Rydel TJ;

XX WPI; 2004-058368/06.  
 DR P-PSDB; ADM93066.  
 XX New lipid acyl hydrolase proteins, useful for inhibiting insect  
 PT infestation of a plant or plant part, for controlling insects, as  
 PT nutritional supplements, or in immunotherapy protocols.  
 XX Example 6; SEQ ID NO 26; 73bp; English.  
 XX The invention relates to an isolated peptide exhibiting lipid acyl  
 CC hydrolyase activity and corn rootworm insect inhibitory bioactivity. The  
 CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation  
 CC of a plant or plant part, for controlling insects (e.g. corn rootworm),  
 CC as nutritional supplements, and in immunotherapy protocols. The present  
 CC sequence represents permutatein plasmid DNA.  
 XX  
 SQ Sequence 1128 BP; 372 A; 202 C; 228 G; 326 T; 0 U; 0 Other;  
 Query Match 91.9%; Score 1036.2; DB 12; Length 1128;  
 Best Local Similarity 99.2%; Pred. No. 9.9e-267;  
 Matches 1041; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 77 AGAGTTTGAATTAATCAATATAGCAATTAAGAGGAGCTGCTGATGATGATGAT 136  
 DB 11 AGAGGCTGAAGCTTACATATACAGCAAAAGAGGAGCTGCTGATGATGATGAT 70  
 QY 137 GTTAGTTATACAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 196  
 DB 71 GTTAGTTATACAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 130  
 QY 197 TACTGCTTTTCAAGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 256  
 DB 131 TACTGCTTTTCAAGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 190  
 QY 257 AACAGGCAACAATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 316  
 DB 191 AACAGGCAACAATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 250  
 QY 317 AGTTGGTGAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 376  
 DB 251 AGTTGGTGAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 310  
 QY 377 AGCTCTAAAGAGGTTTGAATTTGCTCTGATGATGATGATGATGATGATGATGAT 436  
 DB 311 AGCTCTAAAGAGGTTTGAATTTGCTCTGATGATGATGATGATGATGATGATGAT 370  
 QY 437 TTCTTATGACCAAGGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 496  
 DB 371 TTCTTATGACCAAGGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 430  
 QY 497 AATTAGAGGATCATTCGGCTTACCAATTCGAAATTTCTTGAAGACCACTTCAGAAAT 556  
 DB 431 AATTAGAGGATCATTCGGCTTACCAATTCGAAATTTCTTGAAGACCACTTCAGAAAT 490  
 QY 557 GGCAATTAATGACGATGACGATGACGATGACGATGACGATGACGATGACGATGAC 616  
 DB 491 GGCAATTAATGACGATGACGATGACGATGACGATGACGATGACGATGACGATGAC 550  
 QY 617 AGGAGGTTTATGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 676  
 DB 551 AGGAGGTTTATGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 610  
 QY 677 TGGCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 736  
 DB 611 TGGCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 670  
 QY 737 TCAAAATTTTGGCCCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 796  
 DB 671 TCAAAATTTTGGCCCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 730  
 QY 797 TGGAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 856



ID ADM93061 standard; DNA; 1128 BP.  
 XX  
 AC ADM93061;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Permuterin plasmid DNA #2.  
 XX  
 KW lipid acyl hydrolase; corn rootworm; insect infestation; plant;  
 insect control; nutritional supplement; ds; permuterin.  
 XX  
 OS Synthetic.  
 XX  
 PN US6657046-B1.  
 XX  
 PD 02-DEC-2003.  
 XX  
 PF 05-JAN-2001; 2001US-00755274.  
 XX  
 PR 06-JAN-2000; 2000US-0174669P.  
 XX  
 PR 21-JUL-2000; 2000US-0219912P.  
 XX  
 PA (MONS ) MONSANTO TECHNOLOGY LLC.  
 XX  
 PI Alibhai MF, Rydel TJ;  
 XX  
 DR MPI; 2004-058368/06.  
 XX  
 DR P-PSDB; ADM93062.  
 XX  
 PT New lipid acyl hydrolase proteins, useful for inhibiting insect  
 PT infestation of a plant or plant part, for controlling insects, as  
 PT nutritional supplements, or in immunotherapy protocols.  
 XX  
 PS Example 6; SEQ ID NO 22; 73bp; English.  
 XX  
 CC The invention relates to an isolated peptide exhibiting lipid acyl  
 CC hydrolase activity and corn rootworm insect inhibitory bioactivity. The  
 CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation  
 CC of a plant or plant part, for controlling insects (e.g. corn rootworm),  
 CC as nutritional supplements, and in immunotherapy protocols. The present  
 CC sequence represents permuterin plasmid DNA.  
 XX  
 SQ Sequence 1128 BP; 372 A; 202 C; 229 G; 325 T; 0 U; 0 Other;

Query Match 85.4%; Score 963.4; DB 12; Length 1128;  
 Best Local Similarity 99.9%; Pred. No. 3e-247;  
 Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 24 TCATTGAAATTACAAAAAATGCTGCTCTCATTTAGGCACTGGCACTTTCAGAGTTT 83  
 DB 159 TCATTGAAATTACAAAAAATGCTGCTCTCATTTAGGCACTGGCACTTTCAGAGTTT 218  
 QY 84 GATPAAACATATTCAGCAAAAGAGCAGTACCTGAGCTGCTGTATCATTTGATGTT 143  
 DB 219 GATPAAACATATTCAGCAAAAGAGCAGTACCTGAGCTGCTGTATCATTTGATGTT 278  
 QY 144 ATACAGAAATGACTGATGAGCAAGTTCTTACATGACTGATTTATTAACCTTTACTGCT 203  
 DB 279 ATACAGAAATGACTGATGAGCAAGTTCTTACATGACTGATTTATTAACCTTTACTGCT 338  
 QY 204 TTTCAGGCTTTGATTCAAAAAACAATTACCTCAGGGTTCAAGAAAATGCAATTAACAGGC 263  
 DB 339 TTTCAGGCTTTGATTCAAAAAACAATTACCTCAGGGTTCAAGAAAATGCAATTAACAGGC 398  
 QY 264 ACAACTACTGAATGATGATGCTTCTGAGGCTAATATGAAATTAATAGTAAAGTTGCT 323  
 DB 399 ACAACTACTGAATGATGATGCTTCTGAGGCTAATATGAAATTAATAGTAAAGTTGCT 458  
 QY 324 GAAACCTTATTTGAAGAACCAAGTTTCGAAAGACATCTGAAACCTATGAGAGCTCTA 383  
 DB 459 GAAACCTTATTTGAAGAACCAAGTTTCGAAAGACATCTGAAACCTATGAGAGCTCTA 518  
 QY 384 AAGAGGTTTGCAAAATTTGCTCTCTGATAGAGAAACTCCGAGCAACAAAGCTTCTTAT 443

DB 519 AAGAGGTTTGCAAAATTTGCTCTCTGATAGAGAAACTCCGAGCAACAAAGCTTCTTAT 578  
 QY 444 GGACCAAGACAGTTGGAGAAATGATGACTGTTCTTATGATGATGAGAGTGAATTAAG 503  
 DB 579 GGACCAAGACAGTTGGAGAAATGATGACTGTTCTTATGATGATGAGAGTGAATTAAG 638  
 QY 504 GGGATCATTCGGGCTACCATTTCTCGAATTTCTTGAAGCAACTTCAGGAAATGACAAAT 563  
 DB 639 GGGATCATTCGGGCTACCATTTCTCGAATTTCTTGAAGCAACTTCAGGAAATGACAAAT 698  
 QY 564 AATGAGATGCAAGACTTGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 623  
 DB 699 AATGAGATGCAAGACTTGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 758  
 QY 624 TTATTGACTGCTATGATTAAGTACTCCAAATGAAACCAATCGACCTTTGCTGCTGCAAA 683  
 DB 759 TTATTGACTGCTATGATTAAGTACTCCAAATGAAACCAATCGACCTTTGCTGCTGCAAA 818  
 QY 684 GAAATTGTACCTTTTACTTTCGAAACATGAGCCCTCAGATTTTATCTGTAGTCAAAAT 743  
 DB 819 GAAATTGTACCTTTTACTTTCGAAACATGAGCCCTCAGATTTTATCTGTAGTCAAAAT 878  
 QY 744 TTAGGCCCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAACCTTGAAGA 803  
 DB 879 TTAGGCCCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAACCTTGAAGA 938  
 QY 804 ACTGCTGTCATCAAGCTTTGACAGAAAGTTGTCATCTCAAGCTTTGACATCAAAACAAAT 863  
 DB 939 ACTGCTGTCATCAAGCTTTGACAGAAAGTTGTCATCTCAAGCTTTGACATCAAAACAAAT 998  
 QY 864 AAGCCGATTAATTTCTTAAGTCAAAATTTAGCAAACTTCCAGAAATTTGATGATGATGATG 923  
 DB 999 AAGCCGATTAATTTCTTAAGTCAAAATTTAGCAAACTTCCAGAAATTTGATGATGATGATG 1058  
 QY 924 TATGATTAAGTATTTCCAGAGAGGCTCCAAATTTTCTCCGATTAATTTCTTCTTGT 983  
 DB 1059 TATGATTAAGTATTTCCAGAGAGGCTCCAAATTTTCTCCGATTAATTTCTTCTTGT 1118  
 QY 984 ACTAA 988  
 DB 1119 ACTTA 1123

RESULT 7  
 AAH73838  
 ID AAH73838 standard; DNA; 1128 BP.  
 XX  
 AC AAH73838;  
 XX  
 DT 28-SEP-2001 (first entry)  
 XX  
 DE Permuterin protein coding sequence #3.  
 XX  
 KW Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;  
 KW larva growth; lipid acyl hydrolase; insecticide; ds.  
 OS Unidentified.  
 XX  
 PN MO200149834-A2.  
 XX  
 PD 12-JUL-2001.  
 XX  
 PF 05-JAN-2001; 2001MO-US000342.  
 XX  
 PR 06-JAN-2000; 2000US-0174669P.  
 XX  
 PA (MONS ) MONSANTO CO.  
 XX  
 PI Alibhai MF, Astwood JD, McWhorter CA, Sampson HA;  
 XX  
 DR MPI; 2001-441874/47.  
 XX



PT Modified potato patatin proteins with reduced antigenicity, useful as  
 PT insecticides for controlling e.g. round worm and root worm.

PS Example 9; Page 187-188; 223pp; English.

XX The present invention relates to modified potato patatins that maintain  
 CC enzymatic and insecticidal activity but which have reduced allergenicity.  
 CC Groups (especially Tyr) which bind to anti-patatin antibodies were  
 CC identified and glycosylation sites involved in antibody binding were  
 CC removed via site directed mutagenesis. The patatins stunt the growth of  
 CC larvae so that maturation is prevented or delayed. The patatins also have  
 CC non-specific lipid hydrolase activity. The modified patatins are  
 CC also useful for inhibiting the activity of corn root worms.  
 CC Deallergised protein can be used as insecticides, as nutritional  
 CC supplements and as immunising agents. The present sequence was used to  
 CC illustrate the present invention

XX Sequence 1128 BP; 372 A; 202 C; 229 G; 325 T; 0 U; 0 Other;

Query Match 80.6%; Score 909; DB 4; Length 1128;

Best Local Similarity 100.0%; Pred. No. 1.1e-232; Mismatches 0; Indels 0; Gaps 0;

Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TCATTGAAATTAACAAAAAATGCTGCTCTCATTTAGGCACTGGCACTACTTCAAGATT 83  
 DB 213 TCATTGAAATTAACAAAAAATGCTGCTCTCATTTAGGCACTGGCACTACTTCAAGATT 272  
 QY 84 GATPAAAACATATACAGCAAAAGGCGACGTAAGCTGCTGTAACATTGATTTAGTT 143  
 DB 273 GATPAAAACATATACAGCAAAAGGCGACGTAAGCTGCTGTAACATTGATTTAGTT 332  
 QY 144 ATACAGAAATGACTGATGAGCAAGTTCTTACATGACTGATTTACCTTCTTCACTGCT 203  
 DB 333 ATACAGAAATGACTGATGAGCAAGTTCTTACATGACTGATTTACCTTCTTCACTGCT 392  
 QY 204 TTTCAAGCTCTTGAATTCAAAAAACAATTAACCTCAAGGTTCAAGAAATGCAATTAACAGGC 263  
 DB 393 TTTCAAGCTCTTGAATTCAAAAAACAATTAACCTCAAGGTTCAAGAAATGCAATTAACAGGC 452  
 QY 264 ACAACTACTGAATGATGATGCTTCTGAGGCTAATATGAAATTTATAGTCAAGTTGCT 323  
 DB 453 ACAACTACTGAATGATGATGCTTCTGAGGCTAATATGAAATTTATAGTCAAGTTGCT 512  
 QY 324 GAAACCTTATGAGAAACAGGTTCCGAGAGCAATCTGAAACCTTGAAGAGGCTCTA 383  
 DB 513 GAAACCTTATGAGAAACAGGTTCCGAGAGCAATCTGAAACCTTGAAGAGGCTCTA 572  
 QY 384 AAGAGGTTTGCAGAAATGCTCTCTGATGAGAAAGAACTCCGAGCAAAACAAGCTTCTTAT 443  
 DB 573 AAGAGGTTTGCAGAAATGCTCTCTGATGAGAAAGAACTCCGAGCAAAACAAGCTTCTTAT 632  
 QY 444 GACCCAGACAGATGGGAGAAATGCTGCTTCTTATGATTTATGAGAGTGAATTAGA 503  
 DB 633 GACCCAGACAGATGGGAGAAATGCTGCTTCTTATGATTTATGAGAGTGAATTAGA 692  
 QY 504 GGGATCATTCGGGTACCAATTCCTGATTTCTTGAAGCAACTTCAGGAAATGGAACAT 563  
 DB 693 GGGATCATTCGGGTACCAATTCCTGATTTCTTGAAGCAACTTCAGGAAATGGAACAT 752  
 QY 564 AATGCAATGCAAGACTTGCAGATTAATTTGATGATTTATGAGAGAAACAAGTACAGAGT 623  
 DB 753 AATGCAATGCAAGACTTGCAGATTAATTTGATGATTTATGAGAGAAACAAGTACAGAGT 812  
 QY 624 TTAATGACTGCTATGATTAAGTACTCCAAATGAAAAACAATGACCTTGTCTGCTCCAAA 683  
 DB 813 TTAATGACTGCTATGATTAAGTACTCCAAATGAAAAACAATGACCTTGTCTGCTCCAAA 872  
 QY 684 GAAATGTACTCTTTTACTTCTGAGACATGGCCCTCAGATTTTATCTAGTGGTCAAAAT 743  
 DB 873 GAAATGTACTCTTTTACTTCTGAGACATGGCCCTCAGATTTTATCTAGTGGTCAAAAT 932  
 QY 744 TTAGGCCCAAAATATGATGAAAAATATCTTATGCAAGTTCTTCAAGAAAACTTGGAGAA 803

DB 933 TTAGGCCCAAAATATGATGAAAAATATCTTATGCAAGTTCTTCAAGAAAACTTGGAGAA 992  
 QY 804 ACTGTGTGATCAAGCTTTGACAGAAAGTTGTCTATCTCAAGCTTTGACATCAAAACAAT 863  
 DB 993 ACTGTGTGATCAAGCTTTGACAGAAAGTTGTCTATCTCAAGCTTTGACATCAAAACAAT 1052  
 QY 864 AAGCCATAATATTAATCAATTAAGTCAAAATTTAGCAAACTCTCAGAAATGATGTTAAGT 923  
 DB 1053 AAGCCATAATATTAATCAATTAAGTCAAAATTTAGCAAACTCTCAGAAATGATGTTAAGT 1112  
 QY 924 TATGACATA 932  
 DB 1113 TATGACATA 1121

# RESULT 8

ADM93063 standard; DNA; 1128 BP.

AC ADM93063;

DT 03-JUN-2004 (first entry)

DE Permutatein plasmid DNA #3.

KW lipid acyl hydrolase; corn rootworm; insect infestation; plant;

KW insect control; nutritional supplement; ds; permutatein.

OS Synthetic.

PN US6657046-B1.

PD 02-DEC-2003.

PF 05-JAN-2001; 2001US-00755274.

PR 06-JAN-2000; 2000US-0174669P.

PR 21-JUL-2000; 2000US-0219912P.

XX (MONS ) MONSANTO TECHNOLOGY LLC.

XX Ailbhai MF, Rydel TJ;

XX WPI: 2004-058368/06.

XX P-PsDB; ADM93064.

PS New lipid acyl hydrolase proteins, useful for inhibiting insect

PT infestation of a plant or plant part, for controlling insects, as

PT nutritional supplements, or in immunotherapy protocols.

CC Example 6; SEQ ID NO 24; 73pp; English.

CC The invention relates to an isolated peptide exhibiting lipid acyl

CC hydrolyase activity and corn rootworm insect inhibitory bioactivity. The

CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation

CC of a plant or plant part, for controlling insects (e.g. corn rootworm),

CC as nutritional supplements, and in immunotherapy protocols. The present

CC sequence represents permutatein plasmid DNA.

XX Sequence 1128 BP; 372 A; 202 C; 229 G; 325 T; 0 U; 0 Other;

Query Match 80.6%; Score 909; DB 12; Length 1128;

Best Local Similarity 100.0%; Pred. No. 1.1e-232; Mismatches 0; Indels 0; Gaps 0;

Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TCATTGAAATTAACAAAAAATGCTGCTCTCATTTAGGCACTGGCACTACTTCAAGATT 83

DB 213 TCATTGAAATTAACAAAAAATGCTGCTCTCATTTAGGCACTGGCACTACTTCAAGATT 272

QY 84 GATPAAAACATATACAGCAAAAGGCGACGTAAGCTGCTGTAACATTGATTTAGTT 143

DB 273 GATPAAAACATATACAGCAAAAGGCGACGTAAGCTGCTGTAACATTGATTTAGTT 332

QY	14	ATACGAAAAAAGCATGATGACGACAAGTCTTAAACAATGATGATTTACTCTTCACTGCT	203
Db	333	ATACGAAAAATGACTGATGACGACAAGTCTTAAACAATGATGATTTACTCTTCACTGCT	392
QY	204	TTTCAAGCTCTGATTCACAAAAACAATTACCTCAGGGTTCAAGAAATGACATTAACAGGC	263
Db	393	TTTCAAGCTCTGATTCACAAAAACAATTACCTCAGGGTTCAAGAAATGACATTAACAGGC	452
QY	264	ACAACTACTGAAAATGATGATGCTTCTGAGGCTAAATATGAAATTATTTGATCAAGTTGCT	323
Db	453	ACAACTACTGAAAATGATGATGCTTCTGAGGCTAAATATGAAATTATTTGATCAAGTTGCT	512
QY	324	GAAAACCTATGGAAGAAACCAAGTTCCGAGAACAATCCTGAAACCTATGAGGAAGCTCTA	383
Db	513	GAAAACCTATGGAAGAAACCAAGTTCCGAGAACAATCCTGAAACCTATGAGGAAGCTCTA	572
QY	384	AAGAGTTTGGAAAAATTGCTCTCTGATATGAGAAAGAACTCCAGACAAACAAAGCTCTTAT	443
Db	573	AAGAGTTTGGAAAAATTGCTCTCTGATATGAGAAAGAACTCCAGACAAACAAAGCTCTTAT	632
QY	444	GGACCAAGACAGTTGGGAGAAATGATGACTGTTCTTAATTTATGATGAGGTGGAATTAGA	503
Db	633	GGACCAAGACAGTTGGGAGAAATGATGACTGTTCTTAATTTATGATGAGGTGGAATTAGA	692
QY	504	GGGATCATTCGGGCTCAACATCTCGAAATTTCTTGAAGACAACTTCAGAAATGACAT	563
Db	693	GGGATCATTCGGGCTCAACATCTCGAAATTTCTTGAAGACAACTTCAGAAATGACAT	752
QY	564	AATGCAGATGCAAGACTTGCAGATTACTTTGATGTAATTGAGAGAACAAATGACAGAGGT	623
Db	753	AATGCAGATGCAAGACTTGCAGATTACTTTGATGTAATTGAGAGAACAAATGACAGAGGT	812
QY	624	TTATTTGACTGCTATGATATAGTACTTCGAAATGAGAAACAAATGCAACCTTTGCTGCTGCAA	683
Db	813	TTATTTGACTGCTATGATATAGTACTTCGAAATGAGAAACAAATGCAACCTTTGCTGCTGCAA	872
QY	684	GAAATTTGTAACCTTTTATCTTGGAAACATGCGCCCTCAGATTTTAAATCCTAGTGTCAATTT	743
Db	873	GAAATTTGTAACCTTTTATCTTGGAAACATGCGCCCTCAGATTTTAAATCCTAGTGTCAATTT	932
QY	744	TTAGGCCCAAAATATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAACAACTTGAGAA	803
Db	933	TTAGGCCCAAAATATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAACAACTTGAGAA	992
QY	804	ACTGCTGTGCATCAAGCTTTTGAACAGAAATGTGCATCTCAAGCTTTGACATCAAAACAAT	863
Db	993	ACTGCTGTGCATCAAGCTTTTGAACAGAAATGTGCATCTCAAGCTTTGACATCAAAACAAT	1052
QY	864	AAGCCAGTAATATATCTTAAGTCAAAATTTAGCAAACTTCCAGAAATTTGATGCTTAAGTG	923
Db	1053	AAGCCAGTAATATATCTTAAGTCAAAATTTAGCAAACTTCCAGAAATTTGATGCTTAAGTG	1112
QY	924	TATGACATA 932	
Db	1113	TATGACATA 1121	
RESULT 9			
AAH73844			
ID	AAH73844 standard; DNA; 1128 BP.		
XX	AAH73844;		
AC			
XX			
XX	28-SEP-2001 (first entry)		
DE	Permutuin protein coding sequence #5.		
KM	Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;		
KM	larva growth; lipid acyl hydrolase; insecticide; ds.		
XX	Unidentified.		
OS			
XX	WO200149834-A2.		
NN			

12-JUL-2001.  
05-JAN-2001; 2001WO-US000342.  
06-JAN-2000; 2000US-0174669P.  
(MONS ) MONSANTO CO.  
Alibhai MF, Astwood JD, McWherter CA, Sampson HA;  
WPI; 2001-441874/47.  
Modified potato patatin proteins with reduced antigenicity, useful as  
insecticides for controlling e.g. round worm and root worm.  
Example 11; Page 192-193; 223pp; English.  
The present invention relates to modified potato patatins that maintain  
enzymatic and insecticidal activity but which have reduced allergenicity.  
Groups (especially Tyr) which bind to anti-patatin antibodies were  
identified and glycosylation sites involved in antibody binding were  
removed via site directed mutagenesis. The patatins stunt the growth of  
larvae so that maturation is prevented or delayed. The patatins also have  
non-specific lipid acyl hydrolase activity. The modified patatins are  
also useful for inhibiting the activity of corn round worms.  
Deallergensised protein can be used as insecticides, as nutritional  
supplements and as immunising agents. The present sequence was used to  
illustrate the present invention

Query Match	77.9%	Score 879	DB 4	length 1128
Best Local Similarity	99.4%	Pred. No. 1,2e-224		
Matches	882	Conservative	0	Mismatches 5; Indels 0; Gaps 0
QY	239	GGTTCAAGAAAATGCATTAACAGGCACAACACTACTGAAATGGATGATGCTTCTGAGGCTTAA	298	
Db	14	GGCTGAAGCTAATATCATTTAAACAGGCACAACACTACTGAAATGGATGATGCTTCTGAGGCTTAA	73	
QY	299	TATGGAAATTATAGTACACAGTTGGTGAAGAACTTATTTGAAAGAAACCAAGTTTCCGAAGACAA	358	
Db	74	TATGGAAATTATATGATCAAGTTGGTGAAGAACTTATTTGAAAGAAACCAAGTTTCCGAAGACAA	133	
QY	359	TCCGAAACCATATAGAGAGAGCTCTAAAGAGGTTTGCAAAATTTGCTCTGTGATAGAGAA	418	
Db	134	TCTGAAACCTATATAGAGAGAGCTCTAAAGAGGTTTGCAAAATTTGCTCTGTGATAGAGAA	193	
QY	419	ACTCCGAGCAAAACAAGCTTCTTATATGACCAAGACAGTTGGAGAAATGATGACTGTTCT	478	
Db	194	ACTCCGAGCAAAACAAGCTTCTTATATGACCAAGACAGTTGGAGAAATGATGACTGTTCT	253	
QY	479	TAGTATTTGATGAGAGTGGAAATTAAAGGATATATCCGGCTACCAATCTTCGAATTTCTTGA	538	
Db	254	TAGTATTTGATGAGAGTGGAAATTAAAGGATATATCCGGCTACCAATCTTCGAATTTCTTGA	313	
QY	539	AGGACAACCTCAGGAAATGACCAATTAATGACATGACGACAAAGCTTCAGATTACTTGTGATGT	598	
Db	314	AGGACAACCTCAGGAAATGACCAATTAATGACATGACGACAAAGCTTCAGATTACTTGTGATGT	373	
QY	599	AATTGAGAGAACAAATGACAGAGGTTTATTTGACTGTATGTAATGAACTCCAAATGAAAA	658	
Db	374	AATTGAGAGAACAAATGACAGAGGTTTATTTGACTGTATGTAATGAACTCCAAATGAAAA	433	
QY	659	CAATCGAACCTTGGCTGCTGCAAGAAATTTGATACCTTTTACTTCGAAACATGGCCCTCA	718	
Db	434	CAATCGAACCTTGGCTGCTGCAAGAAATTTGATACCTTTTACTTCGAAACATGGCCCTCA	493	
QY	719	GATTTTAAATCTATAGTGGTCAAAATTTTAAAGCCCAAAATATGATGGAAATATCTTATGCA	778	
Db	494	GATTTTAAATCTATAGTGGTCAAAATTTTAAAGCCCAAAATATGATGGAAATATCTTATGCA	553	
QY	779	AGTTCCTTCAAGAAAACCTTGAGAAACTCGTGTGCATCAAGCTTTGACAGAAATTTGTCAAT	838	

Db 554 AGTCTTCAAGAAAACCTGAGAAACTCGGTGCATCAAGCTTGAAGAAAGTTGTCAT 613  
Qy 839 CTCAAGCTTGAATCAAAACAAATAGCCAGTAAATATTCATAGTCAAAATTTAGCAA 898  
Db 614 CTCAAGCTTGAATCAAAACAAATAGCCAGTAAATATTCATAGTCAAAATTTAGCAA 673  
Qy 899 CTCTCCAGAAATGAGATGATAGATGATAGATGATAGATGATAGATGATAGATGATAG 958  
Db 674 CTCTCCAGAAATGAGATGATAGATGATAGATGATAGATGATAGATGATAGATGATAG 733  
Qy 959 ATATTTTCTCCGCAATTAATTTGTTACTAAATAGTAAATAGATGATAGATGATAGAT 1018  
Db 734 ATATTTTCTCCGCAATTAATTTGTTACTAAATAGTAAATAGATGATAGATGATAGAT 793  
Qy 1019 TCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1078  
Db 794 TCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 853  
Qy 1079 AACGAGCTTGACAAAGAGATCCAGATTTGCTTCAATTAGTAAAT 1125  
Db 854 AACGAGCTTGACAAAGAGATCCAGATTTGCTTCAATTAGTAAAT 900

## RESULT 10

ADM93067  
ID ADM93067 standard; DNA: 1128 BP.

AC ADM93067;

DT 03-JUN-2004 (first entry)

DE Permutectin plasmid DNA #5.

XX lipid acyl hydrolase; corn rootworm; insect infestation; plant;  
KM insect control; nutritional supplement; ds; permutectin.

XX Synthetic.

PN US6657046-B1.

PD 02-DEC-2003.

PF 05-JAN-2001; 2001US-00755274.

PR 06-JAN-2000; 2000US-0174669P.

PR 21-JUL-2000; 2000US-0219912P.

XX (MONS ) MONSANTO TECHNOLOGY LLC.

PA Alibhai MF, Rydel TJ;

PI WPI; 2004-058368/06.

DR P-PDSB; ADM93068.

PT New lipid acyl hydrolase proteins, useful for inhibiting insect  
infestation of a plant or plant part, for controlling insects, as

PT nutritional supplements, or in immunotherapy protocols.

PS Example 6; SEQ ID NO 28; 73pp; English.

XX

XX

CC The invention relates to an isolated peptide exhibiting lipid acyl  
hydrolase activity and corn rootworm insect inhibitory bioactivity. The  
lipid acyl hydrolase peptide is useful for inhibiting insect infestation  
of a plant or plant part, for controlling insects (e.g. corn rootworm),  
as nutritional supplements, and in immunotherapy protocols. The present  
sequence represents permutectin plasmid DNA.

CC Sequence 1128 BP; 372 A; 202 C; 229 G; 325 T; 0 U; 0 Other;

Query Match 77.9%; Score 879; DB 12; Length 1128;

Best Local Similarity 99.4%; Pred. No. 1.2e-224;  
Matches 882; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 239 GGTTCAAGAAATGATTAACAGGACAACTAAGAAATGATGATGATGATGATGATGATGATG 298  
Db 14 GGCTGAGAGTAAATGATTAACAGGACAACTAAGAAATGATGATGATGATGATGATGATG 73  
Qy 299 TATGAAATTAATGATCAAGTTGGTGAATACTAATGAAAGAACAGTTTCCGAAGCAA 358  
Db 74 TATGAAATTAATGATCAAGTTGGTGAATACTAATGAAAGAACAGTTTCCGAAGCAA 133  
Qy 359 TCTGAAACCTATGAGGAACTCTAAGAGATTTGCAAAATTTGCTCTGATAGAGAGAA 418  
Db 134 TCTGAAACCTATGAGGAACTCTAAGAGATTTGCAAAATTTGCTCTGATAGAGAGAA 193  
Qy 419 ACTCCAGCAAAACAAAGCTTATGAGACAGGACAGTGGGAGAAATGATGATGATGATG 478  
Db 194 ACTCCAGCAAAACAAAGCTTATGAGACAGGACAGTGGGAGAAATGATGATGATGATG 253  
Qy 479 TAGTATTAATGAGATGAGATTAAGAGGATCAATTCGGCTACATTTCTGAATTTCTTGA 538  
Db 254 TAGTATTAATGAGATGAGATTAAGAGGATCAATTCGGCTACATTTCTGAATTTCTTGA 313  
Qy 539 AGGACAACTTCAGGAAATGACAAATATGATGATGATGATGATGATGATGATGATGATG 598  
Db 314 AGGACAACTTCAGGAAATGACAAATATGATGATGATGATGATGATGATGATGATGATG 373  
Qy 599 AATTGGAGAAACAGTACAGAGGTTTATGATGATGATGATGATGATGATGATGATGATG 658  
Db 374 AATTGGAGAAACAGTACAGAGGTTTATGATGATGATGATGATGATGATGATGATGATG 433  
Qy 659 CAATGACCTTTGCTGCTGCTCCAAAGAAATTTGATCTTTTACTTCCAAATGAGCCCTCA 718  
Db 434 CAATGACCTTTGCTGCTGCTCCAAAGAAATTTGATCTTTTACTTCCAAATGAGCCCTCA 493  
Qy 719 GATTTTAAATCTAGTGTCAAAATTTAGGCCCAAAATATGATGAGAAATATCTTATGCA 778  
Db 494 GATTTTAAATCTAGTGTCAAAATTTAGGCCCAAAATATGATGAGAAATATCTTATGCA 553  
Qy 779 AGTCTTCAAGAAACCTGAGAAACCTGAGGATCAAGCTTTCAGAGATGTCAT 838  
Db 554 AGTCTTCAAGAAACCTGAGAAACCTGAGGATCAAGCTTTCAGAGATGTCAT 613  
Qy 839 CTCAAGCTTGAATCAAAACAAATAGCCAGTAAATATTCATAGTCAAAATTTAGCAA 898  
Db 614 CTCAAGCTTGAATCAAAACAAATAGCCAGTAAATATTCATAGTCAAAATTTAGCAA 673  
Qy 899 CTCTCCAGAAATGAGATGATAGATGATAGATGATAGATGATAGATGATAGATGATAG 958  
Db 674 CTCTCCAGAAATGAGATGATAGATGATAGATGATAGATGATAGATGATAGATGATAG 733  
Qy 959 ATATTTTCTCCGCAATTAATTTGTTACTAAATAGTAAATAGATGATAGATGATAGAT 1018  
Db 734 ATATTTTCTCCGCAATTAATTTGTTACTAAATAGTAAATAGATGATAGATGATAGAT 793  
Qy 1019 TCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1078  
Db 794 TCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 853  
Qy 1079 AACGAGCTTGACAAAGAGATCCAGATTTGCTTCAATTAGTAAAT 1125  
Db 854 AACGAGCTTGACAAAGAGATCCAGATTTGCTTCAATTAGTAAAT 900

## RESULT 11

AAH73819  
ID AAH73819 standard; DNA: 1138 BP.

AC AAH73819;

DT 28-SEP-2001 (first entry)

DE Thermal amplification primer #3.

XX Insecticidal; immunosuppressive; potatato; palatin; enzyme; PCR primer;



```
QY 513 CCGGCTACATTCGCAATTTCTTGAAGACAACCTCAGGAATGACAATTAATGAGAT 572
DB 130 CCGGCTACATTCGCAATTTCTTGAAGACAACCTCAGGAATGACAATTAATGAGAT 189
QY 573 GCAAGACTTGCAATTAATTTGATGATTAATGAGGAACAATGACAGAGTTATTGACT 632
DB 190 GCAAGACTTGCAATTAATTTGATGATTAATGAGGAACAATGACAGAGTTATTGACT 249
QY 633 GCTATGATAGTACTCCAAATGAAAACATTCGACCTTGTGCTGCCAAAGAAATGTA 692
DB 250 GCTATGATAGTACTCCAAATGAAAACATTCGACCTTGTGCTGCCAAAGAAATGTA 309
QY 693 CTTTTTACTTCCAAACATGCGCCCTCAGATTTTAACTCTAGTGTGCAAAATTTTAGGCCA 752
DB 310 CTTTTTACTTCCAAACATGCGCCCTCAGATTTTAACTCTAGTGTGCAAAATTTTAGGCCA 369
QY 753 AAATATGATGAAAATATCTTATGCAAGTTCTTCAGAAAAAATTGAGAAACTCGTGTG 812
DB 370 AAATATGATGAAAATATCTTATGCAAGTTCTTCAGAAAAAATTGAGAAACTCGTGTG 429
QY 813 CATCAAGCTTTGACAGAAAGTTGTCATCTCAAGCTTTGACATCAAAACAAATTAAGCCAGTA 872
DB 430 CATCAAGCTTTGACAGAAAGTTGTCATCTCAAGCTTTGACATCAAAACAAATTAAGCCAGTA 489
QY 873 ATATTCCTAAGTCAAAATTTAGCAAACTCTCCAGAAATTTGATGCTAGATGATGACATA 932
DB 490 ATATTCCTAAGTCAAAATTTAGCAAACTCTCCAGAAATTTGATGCTAGATGATGACATA 549
QY 933 AGTTATTCACAGACAGAGCTCCAAATTTTCTCCGATTAATTCTTGTACTTAATATCT 992
DB 550 AGTTATTCACAGACAGAGCTCCAAATTTTCTCCGATTAATTCTTGTACTTAATATCT 609
QY 993 AGTTATGAGATGAATATGAGTTCAATCTTGTGTGATGCTGTGCTGCTACTGTTGCTGAT 1052
DB 610 AGTTATGAGATGAATATGAGTTCAATCTTGTGTGATGCTGTGCTGCTACTGTTGCTGAT 669
QY 1053 CCGGCGTTATTCACATTAAGCTTGAAGAGAGCTTGACAAAAAGATTCAGAGATTGGCT 1112
DB 670 CCGGCGTTATTCACATTAAGCTTGAAGAGAGCTTGACAAAAAGATTCAGAGATTGGCT 729
QY 1113 TCAATTAGGTAAT 1125
DB 730 TCAATTAGGTCAT 742

RESULT 13
ADM93077
ID ADM93077 standard; DNA; 1158 BP.
XX
AC ADM93077;
XX
DT 03-JUN-2004 (first entry)
XX
DE Potato patatin DNA.
XX
KW lipid acyl hydrolase; corn rootworm; insect infestation; plant;
XX insect control; nutritional supplement; potato; patatin; de; gene.
XX
OS Solanum tuberosum.
XX
PN US6657046-B1.
XX
PD 02-DEC-2003.
XX
PF 05-JAN-2001; 2001US-00755274.
XX
PR 06-JAN-2000; 2000US-0174669P.
XX 21-JUL-2000; 2000US-0219912P.
XX (MONS ) MONSANTO TECHNOLOGY LLC.
PA
XX Alibhai MF, Rydel TJ;
PI
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XX WPI; 2004-058368/06.
DR P-PSDB; ADM93078.
XX
PT New lipid acyl hydrolase proteins, useful for inhibiting insect
PT infestation of a plant or plant part, for controlling insects, as
PT nutritional supplements, or in immunotherapy protocols.
XX
PS Disclosure; SEQ ID NO 38; 73pp; English.
XX
CC The invention relates to an isolated peptide exhibiting lipid acyl
CC hydrolase activity and corn rootworm insect inhibitory bioactivity. The
CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation
CC of a plant or plant part, for controlling insects (e.g. corn rootworm),
CC as nutritional supplements, and in immunotherapy protocols. The present
CC sequence represents a potato patatin DNA.
XX
SQ Sequence 1158 BP; 380 A; 207 C; 221 G; 350 T; 0 U; 0 Other;
XX
Query Match 59.5%; Score 671.4; DB 12; Length 1158;
Best Local Similarity 99.9%; Pred. No. 4.2e-169;
Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 453 CAGTTGGAGAAAATGCTGCTCTTCTAGTATGATGAGAGTGAATTAAGGATCATTT 512
DB 70 CAGTTGGAGAAAATGCTGCTCTTCTAGTATGATGAGAGTGAATTAAGGATCATTT 129
QY 513 CCGGCTACATTCGCAATTTCTTGAAGACAACCTCAGGAATGACATTAATGCAAT 572
DB 130 CCGGCTACATTCGCAATTTCTTGAAGACAACCTCAGGAATGACATTAATGCAAT 189
QY 573 GCAAGACTTGCAATTAATTTGATGATTAATGAGGAACAATGACAGAGTTATTGACT 632
DB 190 GCAAGACTTGCAATTAATTTGATGATTAATGAGGAACAATGACAGAGTTATTGACT 249
QY 633 GCTATGATAGTACTCCAAATGAAAACATTCGACCTTGTGCTGCCAAAGAAATGTA 692
DB 250 GCTATGATAGTACTCCAAATGAAAACATTCGACCTTGTGCTGCCAAAGAAATGTA 309
QY 693 CTTTTTACTTCCAAACATGCGCCCTCAGATTTTAACTCTAGTGTGCAAAATTTTAGGCCA 752
DB 310 CTTTTTACTTCCAAACATGCGCCCTCAGATTTTAACTCTAGTGTGCAAAATTTTAGGCCA 369
QY 753 AAATATGATGAAAATATCTTATGCAAGTTCTTCAGAAAAAATTGAGAAACTCGTGTG 812
DB 370 AAATATGATGAAAATATCTTATGCAAGTTCTTCAGAAAAAATTGAGAAACTCGTGTG 429
QY 813 CATCAAGCTTTGACAGAAAGTTGTCATCTCAAGCTTTGACATCAAAACAAATTAAGCCAGTA 872
DB 430 CATCAAGCTTTGACAGAAAGTTGTCATCTCAAGCTTTGACATCAAAACAAATTAAGCCAGTA 489
QY 873 ATATTCCTAAGTCAAAATTTAGCAAACTCTCCAGAAATTTGATGCTAGATGATGACATA 932
DB 490 ATATTCCTAAGTCAAAATTTAGCAAACTCTCCAGAAATTTGATGCTAGATGATGACATA 549
QY 933 AGTTATTCACAGACAGAGCTCCAAATTTTCTCCGATTAATTCTTGTACTTAATATCT 992
DB 550 AGTTATTCACAGACAGAGCTCCAAATTTTCTCCGATTAATTCTTGTACTTAATATCT 609
QY 993 AGTTATGAGATGAATATGAGTTCAATCTTGTGTGATGCTGTGCTGCTACTGTTGCTGAT 1052
DB 610 AGTTATGAGATGAATATGAGTTCAATCTTGTGTGATGCTGTGCTGCTACTGTTGCTGAT 669
QY 1053 CCGGCGTTATTCACATTAAGCTTGAAGAGAGCTTGACAAAAAGATTCAGAGATTGGCT 1112
DB 670 CCGGCGTTATTCACATTAAGCTTGAAGAGAGCTTGACAAAAAGATTCAGAGATTGGCT 729
QY 1113 TCAATTAGGTAAT 1125
DB 730 TCAATTAGGTCAT 742

RESULT 14
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AAH73854  
 ID AAH73854 standard; DNA; 1161 BP.  
 AC AAH73854;  
 XX  
 XX 28-SEP-2001 (first entry)  
 DT  
 DE Patatin homolog Pat17 coding sequence.  
 XX  
 XX Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;  
 KM larva growth; lipid acyl hydrolase; insecticide; ds.  
 XX  
 OS Solanum tuberosum.  
 XX  
 PN MO200149834-A2.  
 XX  
 PD 12-JUL-2001.  
 XX  
 PF 05-JAN-2001; 2001MO-US000342.  
 XX  
 XX 06-JAN-2000; 2000US-0174669P.  
 XX  
 XX (MONS ) MONSANTO CO.  
 PA  
 PI Alibhai MF, Ashtwood JD, Mcwherter CA, Sampson HA;  
 XX  
 DR WPI; 2001-441874/47.  
 XX  
 PT Modified potato patatin proteins with reduced antigenicity, useful as  
 XX insecticides for controlling e.g. round worm and root worm.  
 XX  
 PS Disclosure; Page 210-211; 223pp; English.  
 XX  
 CC The present invention relates to modified potato patatins that maintain  
 CC enzymatic and insecticidal activity but which have reduced allergenicity.  
 CC Groups (especially Tyr) which bind to anti-patatin antibodies were  
 CC identified and glycosylation sites involved in antibody binding were  
 CC removed via site directed mutagenesis. The patatins stunt the growth of  
 CC larvae so that maturation is prevented or delayed. The patatins also have  
 CC non-specific lipid acyl hydrolase activity. The modified patatins are  
 CC also useful for inhibiting the activity of corn round worms.  
 CC CC Deallegensised protein can be used as insecticides, as nutritional  
 CC supplements and as immunising agents. The present sequence was used to  
 CC illustrate the present invention  
 CC  
 SQ Sequence 1161 BP; 382 A; 207 C; 221 G; 351 T; 0 U; 0 Other;  
 Query Match 59.5%; Score 671.4; DB 4; Length 1161;  
 Best Local Similarity 99.9%; Pred. No. 4.2e-169;  
 Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 453 CAGTTGGAGAAATGCTGCTCTTCTAGATTGATGAGTGGAAATTAGAGGATCATT 512  
 DB 70 CAGTTGGAGAAATGCTGCTCTTCTAGATTGATGAGTGGAAATTAGAGGATCATT 129  
 QY 513 CCGGCTACCATCTTCGATTTCTTGAAGCAACTTCAGAAATGCAATTAATGCAGAT 572  
 DB 130 CCGGCTACCATCTTCGATTTCTTGAAGCAACTTCAGAAATGCAATTAATGCAGAT 189  
 QY 573 GCAAGACTTGACATTAATTGATGATGAGGAAACAGTACAGAGGTTTATGACT 632  
 DB 190 GCAAGACTTGACATTAATTGATGATGAGGAAACAGTACAGAGGTTTATGACT 249  
 QY 633 GCTATGATAGTACTCCAAATGAAACATGACCTTTGCTCTGCGCAAGAAATTGTA 692  
 DB 250 GCTATGATAGTACTCCAAATGAAACATGACCTTTGCTCTGCGCAAGAAATTGTA 309  
 QY 693 CTTTTTACTTGAACATGCGCTCAGATTTTAACTCCTAGTGGTCAATTTTAAAGGCCA 752  
 DB 310 CTTTTTACTTGAACATGCGCTCAGATTTTAACTCCTAGTGGTCAATTTTAAAGGCCA 369  
 QY 753 AATATGATGAAATATCTTATGCAAGTTCTTCAAGAAAACCTTGAGAAATCTCGTGTG 812

DB 370 AATATGATGAAATATCTTATGCAAGTTCTTCAAGAAAACCTTGAGAAATCTCGTGTG 429  
 QY 813 CATCAAGCTTTGACAGAACTTGTCTCATCTCAAGCTTTGACATCAAAACAATAAGCCAGTA 872  
 DB 430 CATCAAGCTTTGACAGAACTTGTCTCATCTCAAGCTTTGACATCAAAACAATAAGCCAGTA 489  
 QY 873 ATATTACCTAAGCAAAATTAGCAAACTCTCCAGAAATTGATGCTAAGATATGACATA 932  
 DB 490 ATATTACCTAAGCAAAATTAGCAAACTCTCCAGAAATTGATGCTAAGATATGACATA 549  
 QY 933 AGTTATTCACAGACAGACACTCCAAATATTTTCCCTCCGCAATTAATTGTAATAACT 992  
 DB 550 AGTTATTCACAGACAGACACTCCAAATATTTTCCCTCCGCAATTAATTGTAATAACT 609  
 QY 993 AGTAATGAGATGATATGATGATTAATCTGTTGATGCTGCTGCTAATCTGTTGAT 1052  
 DB 610 AGTAATGAGATGATATGATGATTAATCTGTTGATGCTGCTGCTAATCTGTTGAT 669  
 QY 1053 CCGGCGTTATTTATCCATTAGCGTTGCAAGACATTTGCAAAAAGATCCAGATTTGCT 1112  
 DB 670 CCGGCGTTATTTATCCATTAGCGTTGCAAGACATTTGCAAAAAGATCCAGATTTGCT 729  
 QY 1113 TCAATTAGGTAAT 1125  
 DB 730 TCAATTAGGTCAT 742  
 RESULT 15  
 ADM93076  
 ID ADM93076 standard; DNA; 1161 BP.  
 XX  
 AC ADM93076;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Heartleaf nightshade patatin homologue Pat17 DNA.  
 XX  
 KM lipid acyl hydrolase; corn rootworm; insect infestation; plant;  
 KM insect control; nutritional supplement; heartleaf nightshade; patatin;  
 XX Pat17; ds; gene.  
 XX  
 OS Solanum cardiophyllum.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1161  
 FT /\*tag= a  
 FT /product= "Pat17"  
 XX  
 PN US6657046-B1.  
 XX  
 PD 02-DEC-2003.  
 XX  
 PF 05-JAN-2001; 2001US-00755274.  
 XX  
 PR 06-JAN-2000; 2000US-0174669P.  
 XX 21-JUL-2000; 2000US-0219912P.  
 XX  
 PA (MONS ) MONSANTO TECHNOLOGY LLC.  
 XX  
 PI Alibhai MF, Rydel TJ;  
 XX  
 DR WPI; 2004-058368/06.  
 DR P-PSDB; ADM93040.  
 XX  
 XX New lipid acyl hydrolase proteins, useful for inhibiting insect  
 PT infestation of a plant or plant part, for controlling insects, as  
 PT nutritional supplements, or in immunotherapy protocols.  
 XX  
 PS Example 1; SEQ ID NO 37; 73pp; English.  
 XX  
 CC The invention relates to an isolated peptide exhibiting lipid acyl  
 CC hydrolase activity and corn rootworm insect inhibitory bioactivity. The  
 CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation

CC of a plant or plant part, for controlling insects (e.g. corn rootworm),  
CC as nutritional supplements, and in immunotherapy protocols. The present  
CC sequence represents the heartleaf nightshade patatin homologue Pac17 DNA.  
XX

Sequence 1161 BP; 382 A; 207 C; 221 G; 351 T; 0 U; 0 Other;

Query Match 59.5%; Score 671.4; DB 12; Length 1161;

Best Local Similarity 99.9%; Pred. No. 4.2e-169;

Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 513 CCGGCTACCAATTCGAAATTTCTGAAGGACAACTCAGGAAATGSAACAATAATGCAAT 572
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Search completed: April 8, 2005, 13:47:26  
Job time : 663 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 13:10:45 ; Search time 3611 Seconds  
(without alignments)  
11890.472 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_est4: \*  
5: gb\_est5: \*  
6: gb\_est6: \*  
7: gb\_est7: \*  
8: gb\_est8: \*  
9: gb\_est9: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	619.8	54.9	813	4	BG351670 130E12 Ma
2	619.8	54.9	813	7	CV471981 45241.1 C
3	619.8	54.9	813	7	CV471846 45073.1 C
4	619.8	54.9	908	7	CV472569 45932.1 C
5	619.8	54.9	950	7	CV470623 43531.1 C
6	619.8	54.9	973	7	CV469887 42645.1 C
7	619.8	54.9	736	4	BG351688 131A01 Ma
8	618.2	54.8	756	4	BG887880 EST513731
9	618.2	54.8	802	4	BG351001 099E05 Ma
10	618.2	54.8	828	4	BG351741 131G03 Ma
11	617.4	54.7	819	7	CV469997 42774.1 C
12	617.2	54.7	741	4	BG351249 088C08 Ma
13	616.8	54.7	780	4	BG351792 132G04 Ma
14	616.6	54.7	700	4	BG887154 EST513005
15	616.4	54.6	795	7	CV286460 66740.1 A
16	616.4	54.6	799	7	CV470839 43787.1 C
17	616.4	54.6	808	7	CV470073 42867.1 C
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20	616.4	54.6	859	7	CV472364 45695.1 C
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22	615.8	54.6	806	7	CV430029 53026.1 A
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25	614.8	54.5	849	7	CV472622 45993.1 C
26	613.8	54.4	835	7	CK859893 30770 In
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43	608.6	54.0	753	7	CV472232 45537.1 C
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#### ALIGNMENTS

RESULT 1  
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DEFINITION 130E12 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA  
ACCESSION BG351670  
VERSION BG351670.1 GI:13180412  
KEYWORDS EST.  
SOURCE Solanum tuberosum (potato)  
ORGANISM Solanum tuberosum  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiales; Solanales; Solanaceae; Solanum.

REFERENCE 1 (bases 1 to 813)  
Crookshanks, M., Emmersen, J., Welinder, K.G. and Nielsen, K.L.  
The potato tuber transcriptome: analysis of 6077 expressed sequence  
tags  
FEBS Lett. 506 (2), 123-126 (2001)

JOURNAL MEDLINE  
PUBMED  
COMMENT Contact: Karen G. Welinder  
Instituit for bioteknologi  
Aalborg Universitet  
Schngaardsholmsvej 49, 9000 Aalborg, Denmark  
Tel: +45 96358467  
Fax: +45 98141808  
Email: kgy@bio.auc.dk  
Sequenced from the 5' end.  
High quality sequence stop: 813  
POLYA=No.

FEATURES  
source location/Qualifiers  
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Query Match 54.9%; Score 619.8; DB 4; Length 813;  
Best Local Similarity 95.2%; Pred. No. 1.2e-150;  
Matches 639; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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RESULT 2
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LOCUS                                  45241.1 Common Scab-Challenged Tubers Solanum tuberosum cDNA clone
DEFINITION
ACCESSION CV471981
VERSION    CV471981.1 GI:53696757
KEYWORDS   EST.
SOURCE      Solanum tuberosum (potato)
ORGANISM    Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 836)
REFERENCE   1. (bases 1 to 836)
AUTHORS    Flihm,B., Rochwell,C., Sardana,R., Griffiths,R., Laque,M., De
            Koeijer,D., Audy,P., Goyer,C., Li,X-Q., Wang-Pruski,G. and Regan,S.
TITLE      Generation of ESTs from common scab-challenged potato tubers
JOURNAL    Unpublished (2004)
COMMENT     Contact: Barry Flihm
            The Canadian Potato Genome Project - BioAtlantech
            921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
            Email: bflim@bioatlantech.mb.ca
            Seq primer: T3.
            Location/Qualifiers
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Site 2: XhoI; supplier: Pathogen-tuberosum var. Shepody, clone
1756, were inoculated with Streptomyces scabiei EF-35. By
applying 1 ml of a spore stock (OD650 = 0.7). Tubers were
placed in trays of sand and watered from the bottom for
the remainder of the experiment. Inoculated tubers were
sampled at 2 days, 1 week, 2 weeks and 4 weeks
post-infection. Harvested tubers were washed in distilled
water, blotted dry, cut into small pieces and frozen in
liquid nitrogen. RNA was isolated from each sample
collection, pooled and used for cDNA library
construction."

ORIGIN
Query Match          54.9%; Score 619.8; DB 7; Length 836;
Best Local Similarity 95.2%; Pred. No. 1,2e-150;
Matches 639; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

455 GTTGGAGAAATGCTGACCTGTTCTAGTATTGATGAGAGTGGAATTGAAGGATCATTC 514
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Db      209 AAGACTTGCAATTCCTGCAATTTCTTGAGAGCAACTTCAGAGAAATGACATTAATGAGATGC 268
QY      635 TATGATGAGTACTCCAAATGAAAAACAATGACCTTTGCTGCTGCCAAGAAATTTGATCC 694
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Db      389 AATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAACTTGAGAAAATCTGCTGCA 448
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[illegible]

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LOCUS		45932.1	Common Scab-Challenged Tubers Solanum tuberosum cDNA clone	
DEFINITION		45932.5,	mRNA sequence.	
ACCESSION		CY472569		
VERSION		CY472569.1	GI:53697345	
KEYWORDS		EST.		
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ORGANISM		Solanum tuberosum		
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		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
		asterids; lamiales; Solanales; Solanaceae; Solanum.		
		1 (bases 1 to 908)		
REFERENCE		Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Laque,M., De		
AUTHORS		Koeper,D., Audy,P., Goyer,C., Li,X-Q., Wang-Pruski,G. and Regan,S.		
JOURNAL		Generation of ESTs from common scab-challenged potato tubers		
COMMENT		Unpublished (2004)		
		Contact: Barry Flinn		
		The Canadian Potato Genome Project - BioAtlantech		
		921 Collage Hill Rd, Fredericton, ON, E3B 6Z9, CANADA		
		Email: bflinn@bioatlantech.nb.ca		
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		from pathogen-free Solanum tuberosum var. Shepody, clone		
		1756, were inoculated with Streptomyces scabei Er-35, by		
		applying 1 ml of a spore stock (OD <sub>650</sub> = 0.7). Tubers were		
		placed in trays of sand and watered from the bottom for		
		the remainder of the experiment. Inoculated tubers were		
		sampled at 2 days, 1 week, 2 weeks and 4 weeks		
		post-infection. Harvested tubers were washed in distilled		
		water, blotted dry cut into small pieces and frozen in		

ORIGIN  
liquid nitrogen. RNA was isolated from each sample collection, pooled and used for cDNA library construction."

Query Match 54.9%; Score 619.8; DB 7; Length 908;  
Best Local Similarity 95.2%; Pred. No. 1.2e-150;  
Matches 639; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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DB GTTGGAGAAATGCTGCTGCTTCTAGTATGAGAGTGAATTAAGAGATCAATTC 111  
QY 515 GCGTACCATTTCTGAATTTCTTGAAGACACTTCAGGAAATGACAAATATGCAATGC 574  
DB GCGTACCATTTCTGAATTTCTTGAAGACACTTCAGGAAATGACAAATATGCAATGC 171  
QY 575 AAGACTTGGAGATTAAGTATGATGAGAGAAACAAGTACAGAGGTTATTTGACTGC 634  
DB AAGACTTGGAGATTAAGTATGATGAGAGAAACAAGTACAGAGGTTATTTGACTGC 231  
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RESULT 5  
LOCUS CVA70623 950 bp mRNA linear EST 01-OCT-2004  
DEFINITION 43531.1 Common Scab-Challenged Tubers Solanum tuberosum cDNA clone  
ACCESSION CVA70623  
VERSION CVA70623.1 GI:53695399  
KEYWORDS EST.  
SOURCE Solanum tuberosum (potato)  
ORGANISM Solanum tuberosum  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiales; Solanales; Solanaceae; Solanum.  
REFERENCE 1 (bases 1 to 950)  
AUTHORS Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Lague,M., De

TITLE Koeper,D., Andy,P., Goyer,C., Li,X-Q., Wang-Pruski,G. and Regan,S.  
JOURNAL Generation of ESTs from common scab-challenged potato tubers  
COMMENT Unpublished (2004)  
Contact: Barry Flinn  
The Canadian Potato Genome Project - BioAtlantech  
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA  
Email: bflinn@biatlantech.nb.ca  
Seq primer: T3.

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from pathogen-free Solanum tuberosum var. Shepody, clone  
1756, were inoculated with Streptomyces scabiei EF-35, by  
applying 1 ml of a spore stock (OD650 = 0.7). Tubers were  
placed in trays of sand and watered from the bottom for  
the remainder of the experiment. Inoculated tubers were  
sampled at 2 days, 1 week, 2 weeks and 4 weeks  
post-infection. Harvested tubers were washed in distilled  
water, blotted dry, cut into small pieces and frozen in  
liquid nitrogen. RNA was isolated from each sample  
collection, pooled and used for cDNA library  
construction."

## ORIGIN

Query Match 54.9%; Score 619.8; DB 7; Length 950;  
Best Local Similarity 95.2%; Pred. No. 1.2e-150;  
Matches 639; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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DB GCGTACCATTTCTGAATTTCTTGAAGACACTTCAGGAAATGACAAATATGCAATGC 187  
QY 575 AAGACTTGGAGATTAAGTATGATGAGAGAAACAATGACAGAGTTTATTTGACTGC 634  
DB AAGACTTGGAGATTAAGTATGATGAGAGAAACAATGACAGAGTTTATTTGACTGC 247  
QY 635 TATGATTAAGTACTCCAAATGAAACAATGACCTTTGCTGCTGCCAAAGAAATTTGACC 694  
DB TATGATTAAGTACTCCAAATGAAACAATGACCTTTGCTGCTGCCAAAGAAATTTGACC 307  
QY 695 TTTTACTTGGAAATGCGCTCAGATTTTAAATCTAGTGTCAATTTTGAAGCCCAAA 754  
DB TTTTACTTGGAAATGCGCTCAGATTTTAAATCTAGTGTCAATTTTGAAGCCCAAT 367  
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QY 935 TTAATTCACAGAGAGAGCTCCAAATATTTCTCCGACATTTGTTTATCTAATCTAG 994  
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QY	995	TAATGAGATGAATATGATGATTCATCTGTTGATGATGCTGTGGTATCATGTTGGATGCC	1054
Db	608	TAATGAGATGAATATGATGATTCATCTGTTGATGATGCTGTGGTATCATGTTGGATGCC	667
QY	1055	GGCGTTATTCATTCATTAGCGTTGCAACGAGACTTGACAAAAGATCCAGCATTTGCTTC	1114
Db	668	GGCGTTATTCATTCCTTAGCGTTGCAACGAGACTTGACAAAAGATCCAGCATTTGCTTC	727
QY	1115	AATTAGGTAAT	1125
Db	728	AATTAGGTAAT	738
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DEFINITION	CV469887	42645, 5'	mRNA sequence.
ACCESSION	CV469887		
VERSION	CV469887.1	GI:53694663	
KEYWORDS	EST.		
SOURCE	Solanum tuberosum (potato)		
ORGANISM	Solanum tuberosum		
REFERENCE	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.		
AUTHORS	Plim, B., Rothwell, C., Sardana, R., Griffiths, R., Laque, M., De Koeijer, D., Andy, P., Goyer, C., Li, X-Q., Wang-Prukski, G. and Regan, S.		
TITLE	Generation of ESTs from common scab-challenged potato tubers		
JOURNAL	Unpublished (2004)		
COMMENT	Contact: Barry Plim The Canadian Potato Genome Project - BioAtlantech 921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA Email: bplim@bioatlantech.nb.ca Seq_primer: T3.		
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	/lab_host="Xl10-Gold"		
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	/note="Vector: pBluescript II SK(+); XR; Site 1: EcoRI; Site 2: XhoI; supplier: Pathogen-challenge series. Tubers from pathogen-free Solanum tuberosum var. Shepody, clone 1756, were inoculated with Streptomyces scabiei EF-35, by applying 1 ml of a spore stock (0.0650 = 0.7). Tubers were placed in trays of sand and watered from the bottom for the remainder of the experiment. Inoculated tubers were sampled at 2 days, 1 week, 2 weeks and 4 weeks post-infection. Harvested tubers were washed in distilled water, blotted dry, cut into small pieces and frozen in liquid nitrogen. RNA was isolated from each sample collection, pooled and used for cDNA library construction."		
ORIGIN			
	Query Match	54.9%	Score 619.8; DB 7; Length 973;
	Best Local Similarity	95.2%	Pred. No. 1.2e-150;
	Matches 639; Conservative 0; Mismatches 32; Indels 0; Gaps 0;		
QY	455	GTGGGAGAAATGCTGACTGTTCTTAGTATGATGAGGTGGAATTAAGGATCATTC	514
Db	68	GTGGGAGAAATGCTGACTGTTCTTAGTATGATGAGGTGGAATTAAGGATCATTC	127
QY	515	GGCTACCAATTCGAAATTCCTGAAGGACAACTTCAGGAAATGACAAATTAAGCAGATGC	574
Db	128	GGCTACCAATTCGAAATTCCTGAAGGACAACTTCAGGAAATGACAAATTAAGCAGATGC	187

Qy		575	AAGCTTCGACGATTA	CTTGATGTAAATTGGAGGAACA	GATACGAGAGTTATTTGACTGC	634	
Db		188	AAGCTTGCAGATTAC	TCTTGATGTAAATTGGAGGAACA	GATACGAGAGTTATTTGACTGC	247	
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Db		248	TATGATAAAGTACTC	CAAAATGAAAACAATGCA	CCCTTGTGCTGCCAAGAATTTGACC	307	
Qy		695	TTTTTACTTGGAAC	ATGCGCCCTCAGATTTT	TAATCCAGTGTGCAATTTT	TAGGCCCAA	754
Db		308	TTTTTACTTGGAAC	ATGCGCCCTCAGATTTT	TAATCCAGTGTGCAATTTT	TAGGCCCAA	367
Qy		755	ATATGATGAAAAAT	ATCTTAGCAAGTTCTTCA	AGAAAAAACTTGAAGAACTCGTGCA	814	
Db		368	GTATGATGAAAAAT	ATTTTCTGCAAGTTCTTCA	AGAAAAAACTTGAAGAACTCGTGCA	427	
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Db		488	ATTCACTAAGTCAA	ATTATTTAGCAAACTTCC	AGAAATTGGATGTAAATGTATGACATAG	547	
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Qy		995	TAATGAGATGAAT	ATATAGTTCATCTTGTGTGATGTG	CTGTGCTACTAGTGTGCTGATCC	1054	
Db		608	TAATGAGATGAAT	ATATAGTTCATCTTGTGTGATGTG	CTGTGCTACTAGTGTGCTGATCC	667	
Qy		1055	GGCGTTATTTATC	ATTAGCGTTGACAGAGACTTGC	CAAAAAGATCOAGCATTTGCTTC	1114	
Db		668	GGCGTTATTTATC	ATTAGCGTTGACAGAGACTTGC	CAAAAAGATCOAGCATTTGCTTC	727	
Qy		1115	AATTAGCTAAT	1125			
Db		728	AATTAGCTAAT	738			
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DEFINITION	131A01 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA sequence.						
ACCESSION	BG351688						
VERSION	BG351688.1		GI:13180430				
KEYWORDS	EST.						
SOURCE	Solanum tuberosum (potato)						
ORGANISM	Solanum tuberosum						
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REFERENCE	1 (bases 1 to 736)						
AUTHORS	Crookshanks,M., Emmersen,J., Wejlander,K.G. and Nielsen,K.L.						
TITLE	The potato tuber transcriptome: analysis of 6077 expressed sequence tags						
JOURNAL	FRES Lett. 506 (2), 123-126 (2001)						
MEDLINE	21475600						
PUBMED	11591384						
COMMENT	Contact: Karen G. Wejlander Institut for bioteknologi Aalborg Universitet Schlegelsholmsvej 49, 9000 Aalborg, Denmark Tel.: +45 96358467 Fax: +45 98141808 Email: kgew@bio.auc.dk Sequenced from the 5' end. High quality sequence stop: 736 POLYA-No.						
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source	Location/Qualifiers						
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Db 674 CGGCTATATTCCTTTCCTTGCGTTGCAACGAACCTTGCAACAGTGAATCCAAATTTGCTTC 733  
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Qy 1115 AATTAGTAT 1125  
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Db 734 AATTAGTAT 744

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DEFINITION  
ACCESSION BG351001 GI:13179727  
VERSION BG351001.1  
KEYWORDS  
SOURCE Solanum tuberosum (potato)  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 802)  
Crookshanks, M., Emmersen, J., Welinder, K.G. and Nielsen, K.L.  
The potato tuber transcriptome: analysis of 6077 expressed sequence  
tags  
FEBS Lett. 506 (2), 123-126 (2001)

JOURNAL  
MEDLINE 21475600  
PUBMED 11591384  
COMMENT Contact: Karen G. Welinder  
Institut for bioteknologi  
Aalborg Universitet  
Sohngaardsholmvej 49, 9000 Aalborg, Denmark  
Tel: +45 96358467  
Fax: +45 98141808  
Email: kgw@bio.auc.dk  
Sequenced from the 5' end.  
High quality sequence stop: 802  
POLYA=No.

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ORIGIN  
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Best Local Similarity 95.1%; Pred. No. 3.1e-150;  
Matches 638; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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Db 127 GGTACCATTCGCAATTTCTTGAAGACAACCTTCAGAAATGACATATATGAGATGC 186  
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DEFINITION  
ACCESSION BG351741  
VERSION BG351741.1 GI:13180483  
KEYWORDS  
SOURCE Solanum tuberosum (potato)  
ORGANISM  
Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 828)  
Crookshanks, M., Emmersen, J., Welinder, K.G. and Nielsen, K.L.  
The potato tuber transcriptome: analysis of 6077 expressed sequence  
tags  
FEBS Lett. 506 (2), 123-126 (2001)

JOURNAL  
MEDLINE 21475600  
PUBMED 11591384  
COMMENT Contact: Karen G. Welinder  
Institut for bioteknologi  
Aalborg Universitet  
Sohngaardsholmvej 49, 9000 Aalborg, Denmark  
Tel: +45 96358467  
Fax: +45 98141808  
Email: kgw@bio.auc.dk  
Sequenced from the 5' end.  
High quality sequence stop: 828  
POLYA=No.

FEATURES  
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OY		755	ATATGATGGAATAAATCTTATGCAAGTCTTCAAGAAAACTTGAGAAACTCGTGTGA	814
Db		372	GTAATGATGGAATAAATCTTCTTCGCAAGTCTTCAAGAAAACTTGAGAAACTCGTGTGA	431
OY		815	TCAAGCTTTTGACAGAACTTGTCTCATCTCAGCTTTGCATCAAAAACAATAAGCAGTAAT	874
Db		432	TCAAGCTTTTGACAGAAATGTGCACTCTCAGCTTTGCATCAAAAACAATAAGCAGTAAT	491
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OY		1055	GGCGTTATATTCATTATGCGTTGCAACGAACTTGCAAAAAGGATCCAGACTTTGCTTC	1114
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ACCESSION	BG351792			
VERSION	BG351792.1	GI:13180534		
KEYWORDS	EST.			
SOURCE	Solanum tuberosum (potato)			
ORGANISM	Solanum tuberosum			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.			
AUTHORS	1 (bases 1 to 700) Crookshanks,M., Emmersen,J., Weinder,K.G. and Nielsen,K.L.			
TITLE	The potato tuber transcriptome: analysis of 6077 expressed sequence tags			
JOURNAL	FEBS Lett. 506 (2), 123-126 (2001)			
MEDLINE	21475600			
PUBMED	11591384			
COMMENT	Contact: Karen G. Weinder Institute for bioteknologi Aalborg Universitet Sohnsgaardsholmsvej 49, 9000 Aalborg, Denmark Tel.: +45 96358467 Fax: +45 98141808 Email: kgw@bio.auc.dk Sequenced from the 5' end. High quality sequence stop: 700 POLYA=No.			
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RESULT 15  
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CV2385460				
66740.1	After-Cooking Darkening	A	Solanum tuberosum	CDNA clone
66740.5	mRNA sequence.			

ACCESSION	CV28646U
VERSION	CV286460.1
KEYWORDS	GI:52567707
SOURCE	EST.
ORGANISM	Solanum tuberosum (potato)
	Solanum tuberosum

REFERENCE  
1 (bases 1 to 795)

**AUTHORS** Flinn, B., Rothwell, C., Sardan, R., Griffiths, R., Jagoe, M., de Koeijer, D., Andy, P., Goyer, C., Li, X.-Q., Wang-Puskis, G., and Regan, S.

**TITLE** Generation of ESTs from mature tubers following 1 month storage at 9 degrees celsius, and 95% relative humidity

**JOURNAL** Unpublished (2004)

**COMMENT**  
Contact: Barry Flinn  
The Canadian Potato Genome Project - BioAtlantic  
921 Collège Hill Rd, Fredericton, ON, E3B 6Z9, CANADA  
Email: bflinn@bioatlantic.nd.ca  
Seq primer: T3.

FEATURES	Location/Qualifiers
source	1. .795

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Site_2: XhoI; supplier: Developmental series; plants from
pathogen-free Solanum tuberosum var. Shenpody, clone 1756,
nuclear stock were grown in a screenhouse under natural
conditions. Mature, harvested tubers were stored in the
dark at 9C, 9% relative humidity for 1 month. The tuber
skin was then removed, and RNA was isolated from the
skinless tubers and used for library construction."

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## ORIGIN

Query Match	54.6%	Score 616.4	DB 7	Length 795
Best Local Similarity	95.7%	Pred. No. 9e-150		
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Db 91 GTTGGAGAAATGGTGACTGTTCTTAGIATGATGGAGGGAATPAGAAGGATCATTC 150

Qy 515 GGGTACCACTTCTCGAATTTCTTGAAGACAACTTCGAAATGCAATATATGCAATG 574

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Qy 635 TATGATAAGTACTCCAAATGAAAACAATGCACCCTTGCGTGTGCGAAAGAAATTGTACC 694

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Qy	932	AAAGTTATTCACAGCAGCAGCGCTCCAAACATATTTTCTCCGCACTTACTTGGTACCTAATAC	991
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DQ 992 TAGTAATGCAATGAATAGTTCACACTGTGTGCTGGTTGCTACTGTTGCTGA 105  
631 TATTATGCAATAAATGAGTTCACACTGTGTGCTGGTTGCTACTGTTGCTGA 690

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[illegible]

Search completed: April 8, 2005, 16:10:22  
Job time : 3615 secs

## ORIGIN

Query Match	54.6%	Score 616.4	DB 7	Length 795
Best Local Similarity	95.7%	Pred. No. 9e-150		
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Db 91 GTTGGAGAAATGGTGACTGTTCTTAGIATGATGGAGGGAATPAGAAGGATCATTC 150

Qy 515 GGGTACCACTTCTCGAATTTCTTGAAGACAACTTCGAAATGCAATATATGCAATGC 574

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6 34  
270

Qy 635 TATGATAAGTACTCCAAATGAAAACAATGCACCCTTGCGTGTGCGAAAGAAATTGTACC 694

Db 271 TATGATAAAGTACTCCAAATGAAAACAATGCACCCTTGCGTGTGCGCAATGAAATTGTACC 330

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Db      |||
301 TGGAAATTATTAAGTCAAGGTTGTAAGAACTTATTAAGAAACCAAGTTCCGAAGACATC
Qy      |||
361 CTGAAACCTTATGAGAGAGCTCTAAGAGGTTTGGCAAAATGCTCTGATAGAGAAAC
Qy      |||
361 CTGAAACCTTATGAGAGAGCTCTAAGAGGTTTGGCAAAATGCTCTGATAGAGAAAC
Db      |||
421 TCCGAGCAAAACAAAGCTTCTTATGAGACGAGACAGTTGGAGAAATGGTGACTGTTCTTA
Qy      |||
421 TCCGAGCAAAACAAAGCTTCTTATGAGACGAGACAGTTGGAGAAATGGTGACTGTTCTTA
Db      |||
481 GTATTTATGAGAGGTTGATTAAGAGGATCAATCCGGCTACCAATCTCGAAATTTCTTGAG
Qy      |||
481 GTATTTATGAGAGGTTGATTAAGAGGATCAATCCGGCTACCAATCTCGAAATTTCTTGAG
Db      |||
541 GACAACTTTCAGAAATGAGCAATATGACAGATGACAGACTTTCAGATTTAGTTGATGAA
Qy      |||
541 GACAACTTTCAGAAATGAGCAATATGACAGATGACAGACTTTCAGATTTAGTTGATGAA
Db      |||
541 GACAACTTTCAGAAATGAGCAATATGACAGATGACAGACTTTCAGATTTAGTTGATGAA
Qy      |||
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Db      |||
601 TTGGAGGACAAAGTACAGAGGTTTATGACAGTGTATGATGATCTTCAATGAAACCA
Qy      |||
661 ATGACCCCTTGGCTGCTGCAAGAAATGATGATCTTCAATGATGATGATGATGATGATG
Qy      |||
661 ATGACCCCTTGGCTGCTGCAAGAAATGATGATCTTCAATGATGATGATGATGATGATG
Db      |||
721 TTTTAAATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Qy      |||
721 TTTTAAATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Db      |||
721 TTTTAAATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Qy      |||
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Db      |||
781 TTCTTCAAGAAAACTTGGAGAAACCTGCTGTGATCAAGCTTTCAGAGAGGTTGATCT
Qy      |||
841 CAAGCTTTCAGATCAAAACAAATGATGATGATGATGATGATGATGATGATGATGATG
Qy      |||
841 CAAGCTTTCAGATCAAAACAAATGATGATGATGATGATGATGATGATGATGATGATG
Db      |||
901 CTCCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Qy      |||
901 CTCCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Db      |||
901 CTCCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Qy      |||
961 ATTTTCTCCGATTAATCTTGTATCTAATACTAGTAATGAGATGATGATGATGATG
Qy      |||
961 ATTTTCTCCGATTAATCTTGTATCTAATACTAGTAATGAGATGATGATGATGATG
Db      |||
1021 TTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Qy      |||
1021 TTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Db      |||
1021 TTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Qy      |||
1081 CGAGACTTTCAGAAACAAAGATTCAGCAATTTGCTTCAATTAAGTAAATGAG
Qy      |||
1081 CGAGACTTTCAGAAACAAAGATTCAGCAATTTGCTTCAATTAAGTAAATGAG
Db      |||
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RESULT 2
US-09-755-274-20
; Sequence 20, Application US/09755274
; Patent No. 6657046
; GENERAL INFORMATION:
; APPLICANT: Alibhai, Murtaza
; APPLICANT: Rydel, Timothy
; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases
; FILE REFERENCE: 38-21 (51842)B
; CURRENT APPLICATION NUMBER: US/09/755, 274
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: synthetic

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; FEATURE:
; NAME/KEY: DNA
; LOCATION: (1)..(1128)
; OTHER INFORMATION: pMON37402 sequence encoding permuterin protein
US-09-755-274-20

Query Match      100.0%; Score 1128; DB 4; Length 1128;
Best Local Similarity 100.0%; Pred. No. 1,9e-307;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      |||
1 TCGAGAAAGAGAGGCTGAAGCTTCAATGATTAACAAAAAATGCTGTTGCTCTCAATTAAG
Db      |||
1 TCGAGAAAGAGAGGCTGAAGCTTCAATGATTAACAAAAAATGCTGTTGCTCTCAATTAAG
Qy      |||
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Db      |||
61 GCACTGGCACTTACTTCAAGGTTGATTAACATATACAGCAAAAGAGGCTGATCTGGA
Qy      |||
121 CTGCTGATCACTTGGATGTTATGATTAACAGAAATGATGATGATGATGATGATGATG
Db      |||
121 CTGCTGATCACTTGGATGTTATGATTAACAGAAATGATGATGATGATGATGATGATG
Qy      |||
181 CTGATTTATTAATCTTCTCACTGCTTTCAAGCTCTGATTCAAAAAACAATTAACCTGAGG
Db      |||
181 CTGATTTATTAATCTTCTCACTGCTTTCAAGCTCTGATTCAAAAAACAATTAACCTGAGG
Qy      |||
241 TTCAAGAAAAATGATTAACAGGACAACTAATGAAATGATGATGATGATGATGATGATG
Db      |||
241 TTCAAGAAAAATGATTAACAGGACAACTAATGAAATGATGATGATGATGATGATGATG
Qy      |||
301 TGGAAATTTATGATCAAGTTGGTGAACCAATTAATGAAACCAAGTTTCCGAAGACATC
Db      |||
301 TGGAAATTTATGATCAAGTTGGTGAACCAATTAATGAAACCAAGTTTCCGAAGACATC
Qy      |||
361 CTGAAACCTTATGAGAGAGCTCTAAGAGGTTTSCAAATTTGCTCTGATAGAGAGAAAC
Db      |||
361 CTGAAACCTTATGAGAGAGCTCTAAGAGGTTTSCAAATTTGCTCTGATAGAGAGAAAC
Qy      |||
421 TCCGAGCAAAACAAAGCTTCTTATGAGACGAGACAGTTGGAGAAATGGTGACTGTTCTTA
Db      |||
421 TCCGAGCAAAACAAAGCTTCTTATGAGACGAGACAGTTGGAGAAATGGTGACTGTTCTTA
Qy      |||
481 GTATTTATGAGAGGTTGATTAAGAGGATCAATCCGGCTACCAATCTCGAAATTTCTTGAG
Db      |||
481 GTATTTATGAGAGGTTGATTAAGAGGATCAATCCGGCTACCAATCTCGAAATTTCTTGAG
Qy      |||
541 GACAACTTTCAGAAATGAGCAATATGACAGATGACAGACTTTCAGATTTAGTTGATGAA
Db      |||
541 GACAACTTTCAGAAATGAGCAATATGACAGATGACAGACTTTCAGATTTAGTTGATGAA
Qy      |||
541 GACAACTTTCAGAAATGAGCAATATGACAGATGACAGACTTTCAGATTTAGTTGATGAA
Db      |||
541 GACAACTTTCAGAAATGAGCAATATGACAGATGACAGACTTTCAGATTTAGTTGATGAA
Qy      |||
601 TTGGAGGACAAAGTACAGAGGTTTATGACAGTGTATGATGATCTTCAATGAAACCA
Db      |||
601 TTGGAGGACAAAGTACAGAGGTTTATGACAGTGTATGATGATCTTCAATGAAACCA
Qy      |||
661 ATGACCCCTTGGCTGCTGCAAGAAATGATGATCTTCAATGATGATGATGATGATGATG
Db      |||
661 ATGACCCCTTGGCTGCTGCAAGAAATGATGATCTTCAATGATGATGATGATGATGATG
Qy      |||
721 TTTTAAATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Db      |||
721 TTTTAAATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Qy      |||
781 TTCTTCAAGAAAACTTGGAGAAACCTGCTGTGATCAAGCTTTCAGAGAGGTTGATCT
Db      |||
781 TTCTTCAAGAAAACTTGGAGAAACCTGCTGTGATCAAGCTTTCAGAGAGGTTGATCT
Qy      |||
841 CAAGCTTTCAGAAATGAGCAATATGACAGATGACAGACTTTCAGATTTAGTTGATGAA
Db      |||
841 CAAGCTTTCAGAAATGAGCAATATGACAGATGACAGACTTTCAGATTTAGTTGATGAA
Qy      |||
901 CTCCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Db      |||
901 CTCCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG

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[illegible]

RESULT 3  
 US-09-755-630B-258  
 ; Sequence 258, Application US/09755630B  
 ; Patent No. 6639054  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ALIBHAI, MURTAZA F.  
 ; APPLICANT: ASTWOOD, JAMES D.  
 ; APPLICANT: SAMPSON, HUGH A.  
 ; APPLICANT: MCWHERTER, CHARLES A.  
 ; TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTATIONS  
 ; FILE REFERENCE: 11899.0217.NPUS00 (WOBT217)  
 ; CURRENT APPLICATION NUMBER: US/09/755.630B  
 ; PRIORITY FILING DATE: 2001-01-05  
 ; PRIOR FILING DATE: 2000-01-06  
 ; NUMBER OF SEQ ID NOS: 295  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 258  
 ; LENGTH: 1128  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic construct  
 ; US-09-755-630B-258

Query Match	91.9%	Score 1036.2	DB 4	Length 1128
Best Local Similarly	99.2%	Pred. No. 1.4e-281		
Matches 1041; Conservative	0	Mismatches 8	Indels 0	Gaps 0

QY	77	AGAGTTTATATAAACAATTACAGCAAAAGAGCAGTACTGGACTGCTGTCATTTAGAT	136
Db	11	AGAGGCTAAGCTACATATTACAGCAAAAGAGGAGCTACTGGACTGCTGTCATTTAGAT	70
QY	137	GTTAGTTATACGAAATGACCTGATGACGACAGTTCTTACATGACGTATTAATTAACCTTTC	196
Db	71	GTTAGTTATACGAAATGACCTGATGACGACAGTTCTTACATGACGTATTAATTAACCTTTC	130
QY	197	TACTGCTTTTCAAGCTCTTGATTCAAAAAACAATTACCTCAGGGTTCAAGAAAATGCATT	256
Db	131	TACTGCTTTTCAAGCTCTTGATTCAAAAAACAATTACCTCAGGGTTCAAGAAAATGCATT	190
QY	257	AACAGGCAACACTACTGAAATGATGATGCTTCTGAGGCTAATATGAAATTATTAGTACA	316
Db	191	AACAGGCAACACTACTGAAATGATGATGCTTCTGAGGCTAATATGAAATTATTAGTACA	250
QY	317	AGTTGCTGAAAACTTATTGGAAGAACCACTTCCGAAAGCAATCCGAAACCTATAGGA	376
Db	251	AGTTGCTGAAAACTTATTGGAAGAACCACTTCCGAAAGCAATCCGAAACCTATAGGA	310
QY	377	AGCTCTAAGAAGGTTGCAAAATTTGCTCTGATAGGAAGAAACTCCAGCAAAACAAG	436
Db	311	AGCTCTAAGAAGGTTGCAAAATTTGCTCTGATAGGAAGAAACTCCAGTCAAAACAAG	370
QY	437	TTCTTATGACCAGGACAGTTGGAGAAATGCTGACTGTTAGTATTGATGAGAGTGG	496
Db	371	TTCTTATGACCAGGACAGTTGGAGAAATGCTGACTGTTAGTATTGATGAGAGTGG	430
QY	497	AATTAGAGGATCATTCGGGCTACCATTTCTCGAATTTCTTGAAAGCAACTTCAGGAAT	556

Db	431	AAATTAGAGGATCANTTCCGGCTACACTTCTCGAATTTCTTGAAGACAACAATTGAGAAAT	490
QY	557	GGACAATATGACAGATGCAAGACTTTGCAATTACTTTGATGTAAATTGGAGAACAAAGTAC	616
Db	491	GGACAATATATGCAATGCAAGACTTTGCAAGATTACTTTGATGTAAATTGGAGAACAAAGTAC	550
QY	617	AGGAGGTTTATGACTGCTATGATTAAGTACTCCAAATGAAAACAATGAGACCTTGTGCTGC	676
Db	551	AGGAGGTTTATGACTGCTATGATTAAGTACTCCAAATGAAAACAATGAGACCTTGTGCTGC	610
QY	677	TGCCAAGAAATTTGACTTTTACTTTCTTGCAACATGAGCCCTCAGATTTTAACTCTAGTGG	736
Db	611	TGCCAAGAAATTTGACTTTTACTTTCTTGCAACATGAGCCCTCAGATTTTAACTCTAGTGG	670
QY	737	TCAAATTTTAGGCCCAAAATTTGATGGAATAATTTCTATGCAAGTTCTTCAAGAAAAACT	796
Db	671	TCAAATTTTAGGCCCAAAATTTGATGGAATAATTTCTATGCAAGTTCTTCAAGAAAAACT	730
QY	797	TGGAGAAACTGCTGTCATCAAGCTTTGACAGAAGTGTCAATCTCAAGCTTTGCATCA	856
Db	731	TGGAGAAACTGCTGTCATCAAGCTTTGACAGAAGTGTCAATCTCAAGCTTTGCATCA	790
QY	857	AACAAATGAGCCAGTAATATTCACTAAGTCAAAATTTAGCAAACTCTCAGAAATTTGATGC	916
Db	791	AACAAATGAGCCAGTAATATTCACTAAGTCAAAATTTAGCAAACTCTCAGAAATTTGATGC	850
QY	917	TAAAGTGTATGACATAAGTATTTCACAGCAGCAGCTCCAAACATATTTTCTCCGCATTA	976
Db	851	TAAAGTGTATGACATAAGTATTTCACAGCAGCAGCTCCAAACATATTTTCTCCGCATTA	910
QY	977	CTTTGTTACTAATPCTAGTATGAGAGTAATGAGTTCAAATCTGTGTGATGGTGCTGT	1036
Db	911	CTTTGTTACTAATPCTAGTATGAGAGTAATGAGTTCAAATCTGTGTGATGGTGCTGT	970
QY	1037	TGCTACTGTGCTGATCCGGCGTTATTTATTCATTAGCGTTTGCAACGAGACTTGCACAAA	1096
Db	971	TGCTACTGTGCTGATCCGGCGTTATTTATTCATTAGCGTTTGCAACGAGACTTGCACAAA	1030
QY	1097	GGATTCAGACATTTGCTTCAATTAGTAAT	1125
Db	1031	GGATTCAGACATTTGCTTCAATTAGTAAT	1059

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RESULT 4
US-09-755-274-26
; Sequence 26, Application US/09755274
; Patent No. 6657046
; GENERAL INFORMATION:
; APPLICANT: Alibhai, Murtaza
; APPLICANT: Rydel, Timothy
; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases
; FILE REFERENCE: 38-21 (51842)B
; CURRENT APPLICATION NUMBER: US/09/755,274
; CURRENT FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: synthetic
; FEATURE:
; NAME/KEY: DNA
; LOCATION: (1)..(1128)
; OTHER INFORMATION: pMON37407 sequence encoding permutoxin protein
US-09-755-274-26

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Query Match	91.9%	Score 1036.2	DB 4	Length 1128
Best Local Similarity	99.28%	Pred. 1.4e-281		
Matches 1041; Conservative	0	Mismatches 8	Indels 0	Gaps 0

  

QY	77	AGAGTTGATTAACATATACGCAAAAGAGCGAGCTACTCGAGCTGCTGATCTGATTTGAT	136
DB	11	AGAGGCTTAACCTCAATATATACGCAAAAGAGCGAGCTACTCGAGCTGCTGATCTGATTTGAT	70

QY	137	GTGATGTAACAGAAAATGACGTGATCGACGAAGTCTTACATGATGATGATTTTACCTTC	196
Db	71	GTTAGTATATACAGAAAATGACTGATGACGACAGTTCTTACATGACTGATTTATACCTTTC	130
QY	197	TACTGCTTTTCAAGCTCTTGATTCAAAAACAATTTACTCAAGGCTTCAAGAAAATGCATTT	256
Db	131	TACTGCTTTTCAAGCTCTTGATTTCAAAAACAATTTACTCAAGGCTTCAAGAAAATGCATTT	190
QY	257	AACAGGCAACACTACTGAAATGAGATGAGCTTCGAGGCTAAATGAAATTTATATGATCA	316
Db	191	AACAGGCAACACTACTGAAATGAGATGAGCTTCGAGGCTAAATGAAATTTATATGATCA	250
QY	317	AGTTGATGAAAACCTATGGAAGAAACAGTTTCCGAAACAACTCTGAAACCTATGAGGA	376
Db	251	AGTTGATGAAAACCTATGGAAGAAACAGTTTCCGAAACAACTCTGAAACCTATGAGGA	310
QY	377	AGCTCTAAGAAGTTCGCAAAATTTGCTCTGATATGAGAAAGAACTCCGACGAAACAAGC	436
Db	311	AGCTCTAAGAAGTTCGCAAAATTTGCTCTGATATGAGAAAGAACTCCGATCAAAACAAGC	370
QY	437	TTCTTATGACACGAGCAGTTGGAGAAATGGTGACTGTCTTGTAGTATGATGAGAGTGG	496
Db	371	TTCTTATGACACGAGCAGTTGGAGAAATGGTGACTGTCTTGTATATGATGAGAGTGG	430
QY	497	AATTAGAGGATCAATCCGGCTACCATTTCTGCAATTTCTTGAAAGCAACTTCAGAAAT	556
Db	431	AATTAGAGGATCAATCCGGCTACCATTTCTGCAATTTCTTGAAAGCAACTTCAGAAAT	490
QY	557	GGACATATATGACATGACAGACTTGCAGATTTACTTATATGATATGAGAGAACAAATAC	616
Db	491	GGACATATATCAGATGACAGCTTGACAGATTTACTTATATGATATGAGAGAACAAATAC	550
QY	617	AGGAGGTTTATGACTGCTATGATATAGATCCCAATGAAAACAATGCACCCTTGCTGC	676
Db	551	AGGAGGTTTATGACTGCTATGATATAGATCCCAATGAAAACAATGCACCCTTGCTGC	610
QY	677	TGCCAAGAAATGTACCTTTTAACTTGCAACATGGCCCTCAGATTTTAAATCCTAGTGG	736
Db	611	TGCCAAGAAATGTACCTTTTAACTTGCAACATGGCCCTCAGATTTTAAATCCTAGTGG	670
QY	737	TCAATTTTAAAGCCCAAAATATGATGAGAAATTTCTTATGCAAGTTCTTCAAGAAAACT	796
Db	671	TCAATTTTAAAGCCCAAAATATGATGAGAAATTTCTTATGCAAGTTCTTCAAGAAAACT	730
QY	797	TGAGAGAACTGTGTCATCAAGCTTTTACAGAAATGTGATCTCAAGCTTTGACATCAA	856
Db	731	TGAGAGAACTGTGTCATCAAGCTTTTACAGAAATGTGATCTCAAGCTTTGACATCAA	790
QY	857	AACAAATAGCCAGTAATATTTCACTAAGTCAAAATTTAGCAAACTCTCCAGAAATGATGC	916
Db	791	AACAAATAGCCAGTAATATTTCACTAAGTCAAAATTTAGCAAACTCTCCAGAAATGATGC	850
QY	917	TAAATATGATACAAATTAATTTACAGACGACAGCTCCAAACATATTTTCCCTCCGACATTA	976
Db	851	TAAATATGATACAAATTAATTTACAGACGACAGCTCCAAACATATTTTCCCTCCGACATTA	910
QY	977	CTTTGTTACTATACTAGTAATGAGAGAAATATAGTTTCAATCTTGTGATGATGCTGT	1038
Db	911	CTTTGTTACTATACTAGTAATGAGAGAAATATAGTTTCAATCTTGTGATGATGCTGT	970
QY	1037	TGCTACTGTGCTGATCCGGCGTTATTTATCCATTTAGCGTTGCAACGAGACTTGCACAAA	1096
Db	971	TGCTACTGTGCTGATCCGGCGTTATTTATCCATTTAGCGTTGCAACGAGACTTGCACAAA	1030
QY	1097	GGATCCAGCATTTGCTCAATTTAGGTAAAT	1125
Db	1031	GGATCCAGCATTTGCTCAATTTAGGTAAAT	1059

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? Patent No. 6639054
? GENERAL INFORMATION:
? APPLICANT: ALIBHAI, MURTAZA F.
? APPLICANT: ASTWOOD, JAMES D.
? APPLICANT: CAMPSON, HUGH A.
? APPLICANT: MCHESTER, CHARLES A.
? TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTINS
? FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
? CURRENT APPLICATION NUMBER: US/09/755,630B
? CURRENT FILING DATE: 2001-01-05
? PRIOR APPLICATION NUMBER: US 60/174,669
? PRIOR FILING DATE: 2000-01-06
? NUMBER OF SEQ ID NOS: 295
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 250
? LENGTH: 1128
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Synthetic construct
? US-09-755-630B-250

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Query Match	85.4%	Score	963.4	DB	4	Length	1128
Best Local Similarity	99.9%	Pred.	No.	4,38-261			
Matches	964	Conservative	0	Mismatches	1	Indels	0
QY	24	TCATTTGAATTA	CAAAAAAAATGCTGTGTTCTCTCATTTAGGCACTGCACTTACAGAGTTT	83			
Db	159	TCATTTGAATTA	CAAAAAAAATGCTGTGTTCTCTCATTTAGGCACTGCACTTACAGAGTTT	218			
QY	84	GATTTAAACATTTAC	GAGAAAGGCGAGTACCTGCGACTGCTGTACATTTGATGTACTT	143			
Db	219	GATTTAAACATTTAC	GAGAAAGGCGAGTACCTGCGACTGCTGTACATTTGATGTACTT	278			
QY	144	ATACAGAAAATGACT	GATGACGAAAGTTCTTACATGACTGATTTATCTTTACTGCT	203			
Db	279	ATACAGAAAATGACT	GATGACGAAAGTTCTTACATGACTGATTTATCTTTACTGCT	338			
QY	204	TTTCAAGCTCTTGAT	TTCAAAAAACAATTACCTCAGGGTTCAAGAAATGATTAACAGGC	263			
Db	339	TTTCAAGCTCTTGAT	TTCAAAAAACAATTACCTCAGGGTTCAAGAAATGATTAACAGGC	398			
QY	264	ACAACTACTGAAAT	GATGATGCTTCTTGAGGCTTAATGAAATTAATGATCAAGTTGCT	323			
Db	399	ACAACTACTGAAAT	GATGATGCTTCTTGAGGCTTAATGAAATTAATGATCAAGTTGCT	458			
QY	324	GAAACCTTATTTGA	AGAAACAGATTCCGAGACAAATCTGAAACCTTATGAGAAAGCTCTA	383			
Db	459	GAAACCTTATTTGA	AGAAACAGATTCCGAGACAAATCTGAAACCTTATGAGAAAGCTCTA	518			
QY	384	AAGAGTTTGCAAA	AATGCTCTCTGATAGGAAGAACTCCGAGCAAAACAAAGCTTCTTAT	443			
Db	519	AAGAGTTTGCAAA	AATGCTCTCTGATAGGAAGAACTCCGAGCAAAACAAAGCTTCTTAT	578			
QY	444	GGACCAAGAACAT	TGGGAGAAATGTTGATCTGTTTGTATTTGATGAGAGTGGAAATTTGA	503			
Db	579	GGACCAAGAACAT	TGGGAGAAATGTTGATCTGTTTGTATTTGATGAGAGTGGAAATTTGA	638			
QY	504	GGGATCAATTCGG	GTACCATTTCTGGAATTTCTTGAAGACAACTTCAAGAAATGGACAAT	563			
Db	639	GGGATCAATTCGG	GTACCATTTCTGGAATTTCTTGAAGACAACTTCAAGAAATGGACAAT	698			
QY	564	AATGCAGATCAAG	ACTTTCAGATTAATTTGGAGAACAAATGACAGAGGT	623			
Db	699	AATGCAGATCAAG	ACTTTCAGATTAATTTGGAGAACAAATGACAGAGGT	758			
QY	624	TTATTTGACTGTAT	GATPAAGTACTCCAAATGAAAACAATGACCCCTTGTCTGTGCCAAA	683			
Db	759	TTATTTGACTGTAT	GATPAAGTACTCCAAATGAAAACAATGACCCCTTGTCTGTGCCAAA	818			
QY	684	GAAATTTGACTCTT	TATCTTCGAAACAGGCGCTTCAGATTTTAAATCCATAGTGCATATTT	743			
Db	819	GAAATTTGACTCTT	TATCTTCGAAACAGGCGCTTCAGATTTTAAATCCATAGTGCATATTT	878			



QY 744 TTAGGCCCAAAATATGATGAAAAATATCTTATGCAAGTTCTTCAAGAAAACTTGGAGAA 803  
Db 879 TTAGGCCCAAAATATGATGAAAAATATCTTATGCAAGTTCTTCAAGAAAACTTGGAGAA 938  
QY 804 ACTGCTGTCATCAAGTTTGGACAGAAAGTTGTCTTCAAGCTTTGACATCAAAACAAT 863  
Db 939 ACTGCTGTCATCAAGTTTGGACAGAAAGTTGTCTTCAAGCTTTGACATCAAAACAAT 998  
QY 864 AAGCCGATATATCTAGTCAAAATTTGGCAAACTCTCAGAAATGAGTGAAGT 923  
Db 999 AAGCCGATATATCTAGTCAAAATTTGGCAAACTCTCAGAAATGAGTGAAGT 1058  
QY 924 TATGACATAAGTTATTCACAGCAGACGCTCAACATATTTCTCCGCAATTAATTGTT 983  
Db 1059 TATGACATAAGTTATTCACAGCAGACGCTCAACATATTTCTCCGCAATTAATTGTT 1118  
QY 984 ACTTA 988  
Db 1119 ACTTA 1123

RESULT 6  
US-09-755-274-22  
; Sequence 22, Application US/09755274  
; Patent No. 6657046  
; GENERAL INFORMATION:  
; APPLICANT: Alibhai, Murtaza  
; APPLICANT: Rydel, Timothy  
; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases  
; FILE REFERENCE: 38-21 (51842)B  
; CURRENT APPLICATION NUMBER: US/09/755,274  
; CURRENT FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patent version 3.0  
; SEQ ID NO 22  
; LENGTH: 1128  
; TYPE: DNA  
; ORGANISM: synthetic  
; FEATURE:  
; NAME/KEY: DNA  
; LOCATION: (1)..(1128)  
; OTHER INFORMATION: pMON37405 sequence encoding permutein protein  
; US-09-755-274-22

Query Match 85.4%; Score 963.4; DB 4; Length 1128;  
Best Local Similarity 99.9%; Pred. No. 4.3e-261;  
Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 24 TCATGTAATTACAAAAAATGCTGTGCTCTCATTTAGGCACTGGCAGTCTTCAAGTTT 83  
Db 159 TCATGTAATTACAAAAAATGCTGTGCTCTCATTTAGGCACTGGCAGTCTTCAAGTTT 218  
QY 84 GATATAACATATACAGCAAAAGAGGAGCTACCTGACCTGCTGACATTTGATTTAGTT 143  
Db 219 GATATAACATATACAGCAAAAGAGGAGCTACCTGACCTGCTGACATTTGATTTAGTT 278  
QY 144 ATACAGAAATGACTGATGACAGCAAGTTCTTACATGACTGATTTATTAACCTTTCTACTGCT 203  
Db 279 ATACAGAAATGACTGATGACAGCAAGTTCTTACATGACTGATTTATTAACCTTTCTACTGCT 338  
QY 204 TTTCAGGCTCTGATTCAAAAAACAATTACCTCAGGGTCAAGAAATGATTAACAGGC 263  
Db 339 TTTCAGGCTCTGATTCAAAAAACAATTACCTCAGGGTCAAGAAATGATTAACAGGC 398  
QY 264 ACAACTACTGAAATGATGATGCTTCTGAGGCTAATATGAAATTTATTAACAAGTTGCT 323  
Db 399 ACAACTACTGAAATGATGATGCTTCTGAGGCTAATATGAAATTTATTAACAAGTTGCT 458  
QY 324 GAAACTTATTTGAAGAAACAGTTTCCGAGAGCAATCTGAAACCTTATGAGAAAGCTCTA 383  
Db 459 GAAACTTATTTGAAGAAACAGTTTCCGAGAGCAATCTGAAACCTTATGAGAAAGCTCTA 518

QY 384 AAGAGTTTGCAAAATTTCTCTCTGATGAGAGAAACTCCGAGCAAAACAAGCTTTTAT 443  
Db 519 AAGAGTTTGCAAAATTTCTCTCTGATGAGAGAAACTCCGAGCAAAACAAGCTTTTAT 578  
QY 444 GGACACGACAGATTGGAGAAATGATGACTGTTCTTATGATATGATGAGAGTGAATTTAGA 503  
Db 579 GGACACGACAGATTGGAGAAATGATGACTGTTCTTATGATATGATGAGAGTGAATTTAGA 638  
QY 504 GGGATCATTCGGGCTACATTTCTGAAATTTCTTGAAGCAAACTTCAAGAAATGACAAT 563  
Db 639 GGGATCATTCGGGCTACATTTCTGAAATTTCTTGAAGCAAACTTCAAGAAATGACAAT 698  
QY 564 AATGACAGTCAAGACTTGCAGATTTACTTATGATGATTTGAGAGAACAGTACAGAGT 623  
Db 699 AATGACAGTCAAGACTTGCAGATTTACTTATGATGATTTGAGAGAACAGTACAGAGT 758  
QY 624 TTATGACTGCTATGATTAAGTACTCCAAATGAAACATGACCTTTGCTGCTGCCAA 683  
Db 759 TTATGACTGCTATGATTAAGTACTCCAAATGAAACATGACCTTTGCTGCTGCCAA 818  
QY 684 GAAATGTACTTTTACTTCTGAAACATGGCCCTCAGATTTTAACTTACGTCGAATTT 743  
Db 819 GAAATGTACTTTTACTTCTGAAACATGGCCCTCAGATTTTAACTTACGTCGAATTT 878  
QY 744 TTAGGCCCAAAATATGATGAAAAATATCTTATGCAAGTTCTTCAAGAAAACTTGGAGAA 803  
Db 879 TTAGGCCCAAAATATGATGAAAAATATCTTATGCAAGTTCTTCAAGAAAACTTGGAGAA 938  
QY 804 ACTGCTGTCATCAAGTTTGGACAGAAAGTTGTCTTCAAGCTTTGACATCAAAACAAT 863  
Db 939 ACTGCTGTCATCAAGTTTGGACAGAAAGTTGTCTTCAAGCTTTGACATCAAAACAAT 998  
QY 864 AAGCCGATATATCTAGTCAAAATTTGGCAAACTCTCAGAAATGAGTGAAGT 923  
Db 999 AAGCCGATATATCTAGTCAAAATTTGGCAAACTCTCAGAAATGAGTGAAGT 1058  
QY 924 TATGACATAAGTTATTCACAGCAGACGCTCAACATATTTCTCCGCAATTAATTGTT 983  
Db 1059 TATGACATAAGTTATTCACAGCAGACGCTCAACATATTTCTCCGCAATTAATTGTT 1118  
QY 984 ACTTA 988  
Db 1119 ACTTA 1123

RESULT 7  
US-09-755-630B-254  
; Sequence 254, Application US/09755630B  
; Patent No. 6639054  
; GENERAL INFORMATION:  
; APPLICANT: ALIBHAI, MURTAZA F.  
; APPLICANT: ASTWOOD, JAMES D.  
; APPLICANT: SAMPSON, HUGH A.  
; APPLICANT: MCWHERTER, CHARLES A.  
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTINS  
; FILE REFERENCE: 11899.0217.NPUS00 (MOBET217)  
; CURRENT APPLICATION NUMBER: US/09/755,630B  
; CURRENT FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 60/174,669  
; PRIOR FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 295  
; SOFTWARE: Patent version 3.0  
; SEQ ID NO 254  
; LENGTH: 1128  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
; US-09-755-630B-254

Query Match 80.6%; Score 909; DB 4; Length 1128;  
Best Local Similarity 100.0%; Pred. No. 9e-246;  
Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TCATTGAATTACAAAAAATGCTGTTGCTCTCAATTAGGCACTGGCACTTCAAGTTT 83  
DB 213 TCATTGAATTACAAAAAATGCTGTTGCTCTCAATTAGGCACTGGCACTTCAAGTTT 272  
QY 84 GATPAAAACATATACAGAAAAGGAGGAGCTACCTGACCTGCTGATCTTGAATGTTAGTT 143  
DB 273 GATPAAAACATATACAGAAAAGGAGGAGCTACCTGACCTGCTGATCTTGAATGTTAGTT 332  
QY 144 ATACAGAAAATGACTGATGAGCAAGTTCTTACATGATGATTAATTAACCTTTTACTGCT 203  
DB 333 ATACAGAAAATGACTGATGAGCAAGTTCTTACATGATGATTAATTAACCTTTTACTGCT 392  
QY 204 TTTCAAGCTTTGATTCAAAAAACAATTAACCTGAGGTTCAAGAAAATGATTAACAGGC 263  
DB 393 TTTCAAGCTTTGATTCAAAAAACAATTAACCTGAGGTTCAAGAAAATGATTAACAGGC 452  
QY 264 ACAACATACGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 323  
DB 453 ACAACATACGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 512  
QY 324 GAAAACTTATTGAAGAAACAGTTTCCGAGACATCTGAAAACCTATGAGAACTCTA 383  
DB 513 GAAAACTTATTGAAGAAACAGTTTCCGAGACATCTGAAAACCTATGAGAACTCTA 572  
QY 384 AAGAGTTTGCAAAATTTGCTCTCTGATGAGAAAGAACTCCGAGCAAAACAAGCTTCTAT 443  
DB 573 AAGAGTTTGCAAAATTTGCTCTCTGATGAGAAAGAACTCCGAGCAAAACAAGCTTCTAT 632  
QY 444 GAGCCAGGACAGTTGGGAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 503  
DB 633 GAGCCAGGACAGTTGGGAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 692  
QY 504 GGGATCATTCGGGCTACCATTTCTGAAATTTCTTGAAGACAACTTCAGAAATGACAT 563  
DB 693 GGGATCATTCGGGCTACCATTTCTGAAATTTCTTGAAGACAACTTCAGAAATGACAT 752  
QY 564 AATGCAATGCAAGACTTGCAGATTAATTGATGATTAATTGAGAGAACATGACAGAGT 623  
DB 753 AATGCAATGCAAGACTTGCAGATTAATTGATGATTAATTGAGAGAACATGACAGAGT 812  
QY 624 TTTATGACGCTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 683  
DB 813 TTTATGACGCTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 872  
QY 684 GAAATTTGACCTTTTACTTGAACATGAGCCCTCAGATTTTAACTTGAATGATTAAT 743  
DB 873 GAAATTTGACCTTTTACTTGAACATGAGCCCTCAGATTTTAACTTGAATGATTAAT 932  
QY 744 TTAGGCCCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAACCTTGAGAA 803  
DB 933 TTAGGCCCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAACCTTGAGAA 992  
QY 804 ACTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 863  
DB 993 ACTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1052  
QY 864 AAGCCAGTAATATTTACTAAGTCAAAATTTAGCAAACTCTCAGAAATGATGATGATGAT 923  
DB 1053 AAGCCAGTAATATTTACTAAGTCAAAATTTAGCAAACTCTCAGAAATGATGATGATGAT 1112  
QY 924 TATGACATA 932  
DB 1113 TATGACATA 1121

## RESULT 8

US-09-755-274-24  
; Sequence 24, Application US/09755274  
; Patent No. 6657046  
; GENERAL INFORMATION:  
; APPLICANT: Alibhai, Murtaza  
; APPLICANT: Rydel, Timothy

; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases  
; FILE REFERENCE: 38-21 (51842)B  
; CURRENT APPLICATION NUMBER: US/09/755,274  
; CURRENT FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patent version 3.0  
; SEQ ID NO 24  
; LENGTH: 1128  
; TYPE: DNA  
; ORGANISM: synthetic  
; FEATURE:  
; NAME/KEY: DNA  
; LOCATION: (1)..(1128)  
; OTHER INFORMATION: pMON37406 sequence encoding permuterin protein  
US-09-755-274-24

Query Match 80.6%; Score 909; DB 4; Length 1128;  
Best Local Similarity 100.0%; Pred. No. 9e-246;  
Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TCATTGAATTACAAAAAATGCTGTTGCTCTCAATTAGGCACTGGCACTTCAAGTTT 83  
DB 213 TCATTGAATTACAAAAAATGCTGTTGCTCTCAATTAGGCACTGGCACTTCAAGTTT 272  
QY 84 GATPAAAACATATACAGAAAAGGAGGAGCTACCTGACCTGCTGATCTTGAATGTTAGTT 143  
DB 273 GATPAAAACATATACAGAAAAGGAGGAGCTACCTGACCTGCTGATCTTGAATGTTAGTT 332  
QY 144 ATACAGAAAATGACTGATGAGCAAGTTCTTACATGATGATTAATTAACCTTTTACTGCT 203  
DB 333 ATACAGAAAATGACTGATGAGCAAGTTCTTACATGATGATTAATTAACCTTTTACTGCT 392  
QY 204 TTTCAAGCTTTGATTCAAAAAACAATTAACCTGAGGTTCAAGAAAATGATTAACAGGC 263  
DB 393 TTTCAAGCTTTGATTCAAAAAACAATTAACCTGAGGTTCAAGAAAATGATTAACAGGC 452  
QY 264 ACAACATACGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 323  
DB 453 ACAACATACGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 512  
QY 504 GGGATCATTCGGGCTACCATTTCTGAAATTTCTTGAAGACAACTTCAGAAATGACAT 563  
DB 693 GGGATCATTCGGGCTACCATTTCTGAAATTTCTTGAAGACAACTTCAGAAATGACAT 752  
QY 564 AATGCAATGCAAGACTTGCAGATTAATTGATGATTAATTGAGAGAACATGACAGAGT 623  
DB 753 AATGCAATGCAAGACTTGCAGATTAATTGATGATTAATTGAGAGAACATGACAGAGT 812  
QY 624 TTTATGACGCTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 683  
DB 813 TTTATGACGCTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 872  
QY 684 GAAATTTGACCTTTTACTTGAACATGAGCCCTCAGATTTTAACTTGAATGATTAAT 743  
DB 873 GAAATTTGACCTTTTACTTGAACATGAGCCCTCAGATTTTAACTTGAATGATTAAT 932  
QY 744 TTAGGCCCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAACCTTGAGAA 803  
DB 933 TTAGGCCCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAACCTTGAGAA 992  
QY 804 ACTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 863



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Db 254 TAAATTTGATGAGGAGGAGTAAATGAGGATCATTCGGCTACCATCTTCGAATTTCTTGA 313
QY 539 AGGACAACTTCAGAAATGACAATAATGACATGCAAGACTTCAGATTACTTTGATGT 598
Db 314 AGGACAACTTCAGAAATGACAATAATGACATGCAAGACTTCAGATTACTTTGATGT 373
QY 599 AATTGAGGAAACAAGTACAGAGGTTTATGACTGCTATGATTAATCTCCAAATGAAA 658
Db 374 AATTGAGGAAACAAGTACAGAGGTTTATGACTGCTATGATTAATCTCCAAATGAAA 433
QY 659 CAATGACCCCTTGTGCTGCTGCAAGAATTTGATACCTTTTACTTGGAACATGGCCCTCA 718
Db 434 CAATGACCCCTTGTGCTGCTGCAAGAATTTGATACCTTTTACTTGGAACATGGCCCTCA 493
QY 719 GATTTTAACTCTAGTGTCAAAATTTTAGCCCAAAATATGATGAAATATCTTAGCA 778
Db 494 GATTTTAACTCTAGTGTCAAAATTTTAGCCCAAAATATGATGAAATATCTTAGCA 553
QY 779 AGTTTTCAGAAAAAATTCGAGAACTGCTGTGCATCAAGCTTTGACAGAGTTGTCTAT 838
Db 554 AGTTTTCAGAAAAAATTCGAGAACTGCTGTGCATCAAGCTTTGACAGAGTTGTCTAT 613
QY 839 CTCAGCTTTGACATCAAAACAATAAGCCAGTAAATTAATCACTAAGTCAAAATTTAGCAA 898
Db 614 CTCAGCTTTGACATCAAAACAATAAGCCAGTAAATTAATCACTAAGTCAAAATTTAGCAA 673
QY 899 CTCCTCAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 958
Db 674 CTCCTCAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 733
QY 959 ATATTTTCTCCGCTACTTCTTGTACTAATACTAGTAATGAGTAATGAGTTCAA 1018
Db 734 ATATTTTCTCCGCTACTTCTTGTACTAATACTAGTAATGAGTAATGAGTTCAA 793
QY 1019 TCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1078
Db 794 TCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 853
QY 1079 AACGAGACTTCGACAAAAGGATCCAGACTTGTCAATTAAGTTAAT 1125
Db 854 AACGAGACTTCGACAAAAGGATCCAGACTTGTCAATTAAGTTAAT 900

RESULT 11
US-09-755-630B-5
; Sequence 5, Application US/09755630B
; Patent No. 6639054
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTTEINS
; CURRENT APPLICATION NUMBER: US/09/755,630B
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1138
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-755-630B-5

Query Match 59.6%; Score 672.2; DB 4; Length 1138;
Best Local Similarity 99.6%; Pred. No. 4,3e-179;
Matches 674; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 449 AGGACAGTTGGAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 508
Db 25 AGCTCAGTTGGGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 84
QY 509 CATTCCGGCTACCATTTCTGAAATTTCTTGAAGACAACTTCAGAAATGACAAATATGCG 568
Db 85 CATTCCGGCTACCATTTCTGAAATTTCTTGAAGACAACTTCAGAAATGACAAATATGCG 144
QY 569 AGATGCAAGCTTCGACATTTACTTTGATGATGATGATGATGATGATGATGATGATGATGAT 628
Db 145 AGATGCAAGCTTCGACATTTACTTTGATGATGATGATGATGATGATGATGATGATGATGAT 204
QY 629 GATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 688
Db 205 GATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 264
QY 689 TGTACCTTTTACTTGAACATGAGCCCTGAGATTTTAAATCTGATGATGATGATGATGATG 748
Db 265 TGTACCTTTTACTTGAACATGAGCCCTGAGATTTTAAATCTGATGATGATGATGATGATG 324
QY 749 CCCAAATATGATGAAAAATCTTATGCAAGTTCTTCAAGAAAACTTGAGAAAACTCG 808
Db 325 CCCAAATATGATGAAAAATCTTATGCAAGTTCTTCAAGAAAACTTGAGAAAACTCG 384
QY 809 TGTGCAATCAAGCTTTGACAGAGTTGTCATCTCAAGCTTTGACATCAAAACAATAAGCC 868
Db 385 TGTGCAATCAAGCTTTGACAGAGTTGTCATCTCAAGCTTTGACATCAAAACAATAAGCC 444
QY 869 AGTAAATATTCATTAATGATCAAACTTCAGAAATGATGATGATGATGATGATGATGATGATG 928
Db 445 AGTAAATATTCATTAATGATCAAACTTCAGAAATGATGATGATGATGATGATGATGATGATG 504
QY 929 CATTAATATTCACAGACAGAGCTCCAAATATTTCTCCGCTACTTGTGTTACTAA 988
Db 505 CATTAATATTCACAGACAGAGCTCCAAATATTTCTCCGCTACTTGTGTTACTAA 564
QY 989 TACTAGTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1048
Db 565 TACTAGTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 624
QY 1049 TGAATCCGGGCTTATTAATCAATTAAGCTTGAACAGACTTCGACAAAAGGATCCAGATT 1108
Db 625 TGAATCCGGGCTTATTAATCAATTAAGCTTGAACAGACTTCGACAAAAGGATCCAGATT 684

QY 1109 TGCTTCATTAAGTTAAT 1125
Db 685 TGCTTCATTAAGTTAAT 701

RESULT 12
US-09-755-630B-1
; Sequence 1, Application US/09755630B
; Patent No. 6639054
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTTEINS
; CURRENT APPLICATION NUMBER: US/09/755,630B
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-09-755-630B-1

Query Match 59.5%; Score 671.4; DB 4; Length 1158;
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LENGTH: 1161  
 TYPE: DNA  
 ORGANISM: Solanum tuberosum  
 US-09-755-630B-285

Query Match 59.5%; Score 671.4; DB 4; Length 1161;  
 Best Local Similarity 99.9%; Pred. No. 7.4e-179;  
 Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 453 CAGTTGGAGAAATGTGACTGTTCTTAGTATGATGAGGTGAATTAAGGATCAT 512
DB 70 CAGTTGGAGAAATGTGACTGTTCTTAGTATGATGAGGTGAATTAAGGATCAT 129
QY 513 CCGGCTACCAATCTCGAATTTCTTGAAGCAACTTCAGAAATGACAAATAATGAGAT 572
DB 130 CCGGCTACCAATCTCGAATTTCTTGAAGCAACTTCAGAAATGACAAATAATGAGAT 189
QY 573 GCAAGCTTGAGATTAATTTGATGATGAGGAGAAAGTACAGAGGTTATTGACT 632
DB 190 GCAAGCTTGAGATTAATTTGATGATGAGGAGAAAGTACAGAGGTTATTGACT 249
QY 633 GCTATGATAGTACTGCAATGAAACAAATGACCCCTTGCTGCTGCAAAAGATTTGAT 692
DB 250 GCTATGATAGTACTGCAATGAAACAAATGACCCCTTGCTGCTGCAAAAGATTTGAT 309
QY 693 CCTTTTACTTGAACATGAGCCCTCAGATTTTAACTAGTGTCAAAATTTAGGCCCA 752
DB 310 CCTTTTACTTGAACATGAGCCCTCAGATTTTAACTAGTGTCAAAATTTAGGCCCA 369
QY 753 AAATATGATGAAATATCTTATGCAAGTCTTCAAGAAAACCTTGAGAAACTCGTG 812
DB 370 AAATATGATGAAATATCTTATGCAAGTCTTCAAGAAAACCTTGAGAAACTCGTG 429
QY 813 CATCAAGCTTTGACAGAAAGTGTCAATCTCAAGCTTTGACATCAAAACAAATAAGCCAGTA 872
DB 430 CATCAAGCTTTGACAGAAAGTGTCAATCTCAAGCTTTGACATCAAAACAAATAAGCCAGTA 489
QY 873 AATATGATGAAATATCTTATGCAAGTCTTCAAGAAAACCTTGAGAAACTCGTG 932
DB 490 AATATGATGAAATATCTTATGCAAGTCTTCAAGAAAACCTTGAGAAACTCGTG 549
QY 933 AGTTATTCACAGACAGACAGTCCACATATTTTCCCGATTAATCTTGTACTAATACT 992
DB 550 AGTTATTCACAGACAGACAGTCCACATATTTTCCCGATTAATCTTGTACTAATACT 609
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DB 610 AGTAATGAGATGATATGATGATCAATCTTGTGATGATGCTGTGCTACTGTTGCTGAT 669
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QY 1113 TCAATTAGGTAAT 1125
DB 730 TCAATTAGGTAAT 742

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RESULT 15  
 US-09-755-274-37  
 Sequence 37, Application US/09755274  
 Patent No. 6657046  
 GENERAL INFORMATION:  
 APPLICANT: Alkhal, Muraza  
 TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydroxylases  
 FILE REFERENCE: 38-21 (51842)B  
 CURRENT APPLICATION NUMBER: US/09/755,274  
 NUMBER OF SEQ ID NOS: 60  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 37  
 LENGTH: 1161

TYPE: DNA  
 ORGANISM: Solanum cardiophyllum  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: (1)..(1161)  
 OTHER INFORMATION: patatin homolog Pat17 nucleic acid and amino acid translation  
 US-09-755-274-37

Query Match 59.5%; Score 671.4; DB 4; Length 1161;  
 Best Local Similarity 99.9%; Pred. No. 7.4e-179;  
 Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 453 CAGTTGGAGAAATGTGACTGTTCTTAGTATGATGAGGTGAATTAAGGATCAT 512
DB 70 CAGTTGGAGAAATGTGACTGTTCTTAGTATGATGAGGTGAATTAAGGATCAT 129
QY 513 CCGGCTACCAATCTCGAATTTCTTGAAGCAACTTCAGAAATGACAAATAATGAGAT 572
DB 130 CCGGCTACCAATCTCGAATTTCTTGAAGCAACTTCAGAAATGACAAATAATGAGAT 189
QY 573 GCAAGCTTGAGATTAATTTGATGATGAGGAGAAAGTACAGAGGTTATTGACT 632
DB 190 GCAAGCTTGAGATTAATTTGATGATGAGGAGAAAGTACAGAGGTTATTGACT 249
QY 633 GCTATGATAGTACTGCAATGAAACAAATGACCCCTTGCTGCTGCAAAAGATTTGAT 692
DB 250 GCTATGATAGTACTGCAATGAAACAAATGACCCCTTGCTGCTGCAAAAGATTTGAT 309
QY 693 CCTTTTACTTGAACATGAGCCCTCAGATTTTAACTAGTGTCAAAATTTAGGCCCA 752
DB 310 CCTTTTACTTGAACATGAGCCCTCAGATTTTAACTAGTGTCAAAATTTAGGCCCA 369
QY 753 AAATATGATGAAATATCTTATGCAAGTCTTCAAGAAAACCTTGAGAAACTCGTG 812
DB 370 AAATATGATGAAATATCTTATGCAAGTCTTCAAGAAAACCTTGAGAAACTCGTG 429
QY 813 CATCAAGCTTTGACAGAAAGTGTCAATCTCAAGCTTTGACATCAAAACAAATAAGCCAGTA 872
DB 430 CATCAAGCTTTGACAGAAAGTGTCAATCTCAAGCTTTGACATCAAAACAAATAAGCCAGTA 489
QY 873 AATATGATGAAATATCTTATGCAAGTCTTCAAGAAAACCTTGAGAAACTCGTG 932
DB 490 AATATGATGAAATATCTTATGCAAGTCTTCAAGAAAACCTTGAGAAACTCGTG 549
QY 933 AGTTATTCACAGACAGACAGTCCACATATTTTCCCGATTAATCTTGTACTAATACT 992
DB 550 AGTTATTCACAGACAGACAGTCCACATATTTTCCCGATTAATCTTGTACTAATACT 609
QY 993 AGTAATGAGATGATATGATGATCAATCTTGTGATGATGCTGTGCTACTGTTGCTGAT 1052
DB 610 AGTAATGAGATGATATGATGATCAATCTTGTGATGATGCTGTGCTACTGTTGCTGAT 669
QY 1053 CCGGCGTTATTTATCCATTAAGCGTTGACACGAGACTTGCACAAAAGATCCAGCATTTGCT 1112
DB 670 CCGGCGTTATTTATCCATTAAGCGTTGACACGAGACTTGCACAAAAGATCCAGCATTTGCT 729
QY 1113 TCAATTAGGTAAT 1125
DB 730 TCAATTAGGTAAT 742

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 Job time : 237 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 15:10:06 ; Search time 686 Seconds  
(without alignments)  
9964.554 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1128	100.0	1128	10	US-09-755-630A-246 Sequence 246, App
2	1128	100.0	1128	18	US-10-658-180-246 Sequence 246, App
3	1128	100.0	1128	18	US-10-682-011-20 Sequence 20, App
4	1036.2	91.9	1128	10	US-09-755-630A-258 Sequence 258, App
5	1036.2	91.9	1128	18	US-10-658-180-258 Sequence 258, App
6	1036.2	91.9	1128	18	US-10-682-011-26 Sequence 26, App
7	963.4	85.4	1128	10	US-09-755-630A-250 Sequence 250, App
8	963.4	85.4	1128	18	US-10-658-180-250 Sequence 250, App
9	963.4	85.4	1128	18	US-10-682-011-22 Sequence 22, App
10	909	80.6	1128	10	US-09-755-630A-254 Sequence 254, App
11	909	80.6	1128	18	US-10-658-180-254 Sequence 254, App

12	909	80.6	1128	18	US-10-682-011-24 Sequence 24, App
13	879	77.9	1128	10	US-09-755-630A-262 Sequence 262, App
14	879	77.9	1128	18	US-10-658-180-262 Sequence 262, App
15	879	77.9	1128	18	US-10-682-011-28 Sequence 28, App
16	672.2	59.6	1128	10	US-09-755-630A-5 Sequence 5, App
17	672.2	59.6	1128	18	US-10-658-180-5 Sequence 5, App
18	671.4	59.5	1128	10	US-09-755-630A-1 Sequence 1, App
19	671.4	59.5	1128	18	US-10-658-180-1 Sequence 1, App
20	671.4	59.5	1128	18	US-10-682-011-38 Sequence 38, App
21	671.4	59.5	1128	10	US-09-755-630A-285 Sequence 285, App
22	671.4	59.5	1128	18	US-10-658-180-285 Sequence 285, App
23	671.4	59.5	1128	10	US-10-682-011-37 Sequence 37, App
24	652.4	57.8	1128	18	US-09-755-630A-270 Sequence 270, App
25	652.4	57.8	1128	10	US-10-658-180-270 Sequence 270, App
26	652.4	57.8	1128	18	US-10-682-011-32 Sequence 32, App
27	616	54.6	1128	10	US-09-755-630A-274 Sequence 274, App
28	616	54.6	1128	18	US-10-658-180-274 Sequence 274, App
29	616	54.6	1128	18	US-10-682-011-34 Sequence 34, App
30	390.6	34.6	1128	10	US-09-755-630A-264 Sequence 264, App
31	390.6	34.6	1128	18	US-10-658-180-264 Sequence 264, App
32	390.6	34.6	1128	18	US-10-682-011-30 Sequence 30, App
33	194	17.2	1009	17	US-10-424-599-466 Sequence 466, App
34	185.2	16.4	276	17	US-10-417-280A-50 Sequence 50, App
35	149.2	13.2	1245	9	US-09-938-842A-2546 Sequence 2546, App
36	149.2	13.2	1245	11	US-09-938-842A-2546 Sequence 2546, App
37	143	12.7	1164	18	US-10-437-963-75340 Sequence 75340, App
38	140.8	12.5	1170	14	US-10-034-937-11 Sequence 11, App
39	140.8	12.5	1170	14	US-10-034-937-11 Sequence 11, App
40	139.6	12.4	1170	14	US-10-034-937-15 Sequence 15, App
41	139.6	12.4	1170	14	US-10-034-937-19 Sequence 19, App
42	139.2	12.3	1161	14	US-10-034-937-1 Sequence 1, App
43	139.2	12.3	1170	14	US-10-034-937-25 Sequence 25, App
44	139.2	12.3	1170	14	US-10-034-937-27 Sequence 27, App
45	139.2	12.3	1170	14	US-10-034-937-29 Sequence 29, App

## ALIGNMENTS

RESULT 1  
US-09-755-630A-246  
; Sequence 246, Application US/09755630A  
; Publication No. US20030194399A1  
; GENERAL INFORMATION:  
; APPLICANT: ALTBHAI, MURTAZA F.  
; APPLICANT: ASTWOOD, JAMES D.  
; APPLICANT: SAMPSON, HUGH A.  
; APPLICANT: MCWHERTER, CHARLES A.  
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTINS  
; FILE REFERENCE: 11899.0217.NPUS00 (MORT217)  
; CURRENT APPLICATION NUMBER: US/09/755.630A  
; CURRENT FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 60/174,669  
; PRIOR FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 293  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 246  
; LENGTH: 1128  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-09-755-630A-246

Query Match 100.0%; Score 1128; DB 10; Length 1128;  
Best Local Similarity 100.0%; Pred. No. 2,8e-276;  
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGAGAAAAGAGGCTGAGCTTCATGATTAACAAAAGCTGCTCTCATAG 60  
DB 1 TCGAGAAAAGAGGCTGAGCTTCATGATTAACAAAAGCTGCTCTCATAG 60  
QY 61 GCACTGCACACTACTCAGAGTTGATTAACATATACAGCAAGAGGACGACTACTGA 120

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Db 61 GCACTGCACTACTCTAGAGTTTGATTAACATATACAGAAAGGCGCACTACGGA 120
QY 121 CTGCTGTAACCTTGTAGTATGATTAACAGAAATGACTGATGAGCAAGTTCTTAACATGA 180
Db 121 CTGCTGTAACCTTGTAGTATGATTAACAGAAATGACTGATGAGCAAGTTCTTAACATGA 180
QY 181 CTGATTAATTAACCTTTCTACTGCTTTTCAAGCTCTGATTCGAAATTAACCTCAGGG 240
Db 181 CTGATTAATTAACCTTTCTACTGCTTTTCAAGCTCTGATTCGAAATTAACCTCAGGG 240
QY 241 TTCAAAAAATGATTAACAGGCAACACTAATGATGATGCTTCTGAGGCTTAATA 300
Db 241 TTCAAAAAATGATTAACAGGCAACACTAATGATGATGCTTCTGAGGCTTAATA 300
QY 301 TGGAAATTAATGATTAACAGGCAACACTAATGATGATGCTTCTGAGGCTTAATA 360
Db 301 TGGAAATTAATGATTAACAGGCAACACTAATGATGATGCTTCTGAGGCTTAATA 360
QY 361 CTGAAACCTATAGAGAGCTCTAAGAGGTTTGCAAAATGCTCTGATGAGAGAAAC 420
Db 361 CTGAAACCTATAGAGAGCTCTAAGAGGTTTGCAAAATGCTCTGATGAGAGAAAC 420
QY 421 TCCGACCAAAACAAAGCTCTTATGACACAGACAGTTGGAGAAATGGTACCTTTA 480
Db 421 TCCGACCAAAACAAAGCTCTTATGACACAGACAGTTGGAGAAATGGTACCTTTA 480
QY 481 GATATGATGAGGTGGAATTAAGAGGATCACTCCGGCTACATTCGAAATTTCTGAAAG 540
Db 481 GATATGATGAGGTGGAATTAAGAGGATCACTCCGGCTACATTCGAAATTTCTGAAAG 540
QY 541 GACAACTTCAGAAATGACAAATATGACAGATGCAAGACTTGCAATTAATCTTATGATGA 600
Db 541 GACAACTTCAGAAATGACAAATATGACAGATGCAAGACTTGCAATTAATCTTATGATGA 600
QY 601 TTGAGAGAAACAACTGACAGAGGTTTATGACCTGATGATGATGCTCCAAATGAAAC 660
Db 601 TTGAGAGAAACAACTGACAGAGGTTTATGACCTGATGATGATGCTCCAAATGAAAC 660
QY 661 ATGACCCCTTGTGCTGCGCAAAAGATGATGCTTTTATCTGAAATGAGGCTCAGA 720
Db 661 ATGACCCCTTGTGCTGCGCAAAAGATGATGCTTTTATCTGAAATGAGGCTCAGA 720
QY 721 TTTTAAATCTAGTGTCAAAATTTAGGCCCAAAATATGATGAGAAATATCTTATGCAAG 780
Db 721 TTTTAAATCTAGTGTCAAAATTTAGGCCCAAAATATGATGAGAAATATCTTATGCAAG 780
QY 781 TTCTTCAAGAAAACTTGAGAAATCTGCTGATCAAGCTTTGACAGAAAGTTGTCATCT 840
Db 781 TTCTTCAAGAAAACTTGAGAAATCTGCTGATCAAGCTTTGACAGAAAGTTGTCATCT 840
QY 841 CAGGCTTTGACATCAAAACAAATATGACAGATGATGATGCTTCAATGATGCAAACT 900
Db 841 CAGGCTTTGACATCAAAACAAATATGACAGATGATGATGCTTCAATGATGCAAACT 900
QY 901 CTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
Db 901 CTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
QY 961 ATTTTCTCGCATTAATTTGATTAATTAATGATGATGATGATGATGATGATGATGATG 1020
Db 961 ATTTTCTCGCATTAATTTGATTAATTAATGATGATGATGATGATGATGATGATGATG 1020
QY 1021 TTGTTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1021 TTGTTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 CGAGACTTGACAAAGATCCAGACTTGGCTTCAATTAAGTATGAG 1128
Db 1081 CGAGACTTGACAAAGATCCAGACTTGGCTTCAATTAAGTATGAG 1128
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RESULT 2

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US-10-658-180-246
; Sequence 246, Application US/10658180
; Publication No. US20040216187A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURPAZ A.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMBSON, HUGH A.
; APPLICANT: MCWHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTINS
; FILE REFERENCE: 11899.0217.DVUS02
; CURRENT APPLICATION NUMBER: US/10/658,180
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US 09/755,630
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 246
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-658-180-246

Query Match 100.0%; Score 1128; DB 18; Length 1128;
Best Local Similarity 100.0%; Pred. No. 2,8e-276;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGAAAAAGAGAGCTGAAAGCTTCAATTAACAAAAATGCTGCTCTCATTTAG 60
Db 1 TCAGAAAAAGAGAGCTGAAAGCTTCAATTAACAAAAATGCTGCTCTCATTTAG 60
QY 61 GCACTGCACTACTCTAGAGTTTGATTAACATATACAGAAAGGCGCACTACGGA 120
Db 61 GCACTGCACTACTCTAGAGTTTGATTAACATATACAGAAAGGCGCACTACGGA 120
QY 121 CTGCTGTAACCTTGTAGTATGATTAACAGAAATGACTGATGAGCAAGTTCTTAACATGA 180
Db 121 CTGCTGTAACCTTGTAGTATGATTAACAGAAATGACTGATGAGCAAGTTCTTAACATGA 180
QY 181 CTGATTAATTAACCTTTCTACTGCTTTTCAAGCTCTGATTCGAAATTAACCTCAGGG 240
Db 181 CTGATTAATTAACCTTTCTACTGCTTTTCAAGCTCTGATTCGAAATTAACCTCAGGG 240
QY 241 TTCAAAAAATGATTAACAGGCAACACTAATGATGATGCTTCTGAGGCTTAATA 300
Db 241 TTCAAAAAATGATTAACAGGCAACACTAATGATGATGCTTCTGAGGCTTAATA 300
QY 301 TGGAAATTAATGATTAACAGGCAACACTAATGATGATGCTTCTGAGGCTTAATA 360
Db 301 TGGAAATTAATGATTAACAGGCAACACTAATGATGATGCTTCTGAGGCTTAATA 360
QY 361 CTGAAACCTATAGAGAGCTCTAAGAGGTTTGCAAAATGCTCTGATGAGAGAAAC 420
Db 361 CTGAAACCTATAGAGAGCTCTAAGAGGTTTGCAAAATGCTCTGATGAGAGAAAC 420
QY 421 TCCGACCAAAACAAAGCTCTTATGACACAGACAGTTGGAGAAATGGTACCTTTA 480
Db 421 TCCGACCAAAACAAAGCTCTTATGACACAGACAGTTGGAGAAATGGTACCTTTA 480
QY 481 GATATGATGAGGTGGAATTAAGAGGATCACTCCGGCTACATTCGAAATTTCTGAAAG 540
Db 481 GATATGATGAGGTGGAATTAAGAGGATCACTCCGGCTACATTCGAAATTTCTGAAAG 540
QY 541 GACAACTTCAGAAATGACAAATATGACAGATGCAAGACTTGCAATTAATCTTATGATGA 600
Db 541 GACAACTTCAGAAATGACAAATATGACAGATGCAAGACTTGCAATTAATCTTATGATGA 600
QY 601 TTGAGAGAAACAACTGACAGAGGTTTATGACCTGATGATGATGCTCCAAATGAAAC 660
Db 601 TTGAGAGAAACAACTGACAGAGGTTTATGACCTGATGATGATGCTCCAAATGAAAC 660
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Qy	661	ATGACCCCTTGCAGTCGCAAGAAATTTGACCTTTTATCTTGCAACATGGCCCTCAGA	720
Db	661	ATGACCCCTTGCAGTCGCAAGAAATTTGACCTTTTATCTTGCAACATGGCCCTCAGA	720
Qy	721	TTTTTAATCCTAGTGTCAAAATTTTAGGCCCAAAATATGATGAAAATATCTTATGCAAG	780
Db	721	TTTTTAATCCTAGTGTCAAAATTTTAGGCCCAAAATATGATGAAAATATCTTATGCAAG	780
Qy	781	TTCTTCAAGAAAACTTGAGAAACTCGTGTGCATCAAGCTTTGACAGAGTGTCACT	840
Db	781	TTCTTCAAGAAAACTTGAGAAACTCGTGTGCATCAAGCTTTGACAGAGTGTCACT	840
Qy	841	CAAGCTTTGCATCAAAAACAATAAGCCAGTAATATTCATAAGTCAAAATTTAGCAAACT	900
Db	841	CAAGCTTTGCATCAAAAACAATAAGCCAGTAATATTCATAAGTCAAAATTTAGCAAACT	900
Qy	901	CTCCAGAAATTTGAGTGTCTAAGATGTATGTACATTAAGTATTTCCACAGCAGACGTCCAACAT	960
Db	901	CTCCAGAAATTTGAGTGTCTAAGATGTATGTACATTAAGTATTTCCACAGCAGACGTCCAACAT	960
Qy	961	ATTTTCCCTCCGCATCTACTTGTATCTAATTAAGTAATGAGATGAATATGAGTTCATTC	1020
Db	961	ATTTTCCCTCCGCATCTACTTGTATCTAATTAAGTAATGAGATGAATATGAGTTCATTC	1020
Qy	1021	TTGTTGATGTGTCTGTTCCTACTGTGTCTGATCCGGCGTTATTAATCAATTAGCGTTGCAA	1080
Db	1021	TTGTTGATGTGTCTGTTCCTACTGTGTCTGATCCGGCGTTATTAATCAATTAGCGTTGCAA	1080
Qy	1081	CGAGACTTGCACAAAAGAGATCCAGCATTTTGCTCAATTAGGTAAATGAG	1128
Db	1081	CGAGACTTGCACAAAAGAGATCCAGCATTTTGCTCAATTAGGTAAATGAG	1128

QY	1	TCGAGAAAAGAGAGGCTGAGGCTTCATTCGAAATTCACAAAAAATGCTGTGGCTCATTTAG	60
Db	1	TCGAGAAAAGAGAGGCTGAGGCTTCATTCGAAATTCACAAAAAATGCTGTGGCTCATTTAG	60
QY	61	GCACTGGCACTACTTCAGAGTTTGATATAAACAATATACGCAAAAAGAGCAGCTACTCGGA	120
Db	61	GCACTGGCACTACTTCAGAGTTTGATATAAACAATATACGCAAAAAGAGCAGCTACTCGGA	120
QY	121	CTGCTGTACATTGGATGTTAGTTATATACAGAAATATGACTGATGACGCAAGTTCTTACATGA	180

Query Match 100.0%; Score 1128; DB 18; Length 1128;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-276;  
 Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-682-011-20 sequence encoding permutoxin protein  
 US-10-682-011-20  
 : Sequence 20, Application US/10682011  
 : Publication No. US20040253699A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Alibhai, Murtaza  
 : APPLICANT: Rydel, Timothy  
 : TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases  
 : FILE REFERENCE: 38-21 (51842)B  
 : CURRENT APPLICATION NUMBER: US/10/682,011  
 : CURRENT FILING DATE: 2003-10-09  
 : PRIOR APPLICATION NUMBER: US/09/755,274  
 : PRIOR FILING DATE: 2001-01-05  
 : NUMBER OF SEQ ID NOS: 60  
 : SOFTWARE: PatentIn version 3.0  
 : SEQ ID NO 20  
 : LENGTH: 1128  
 : TYPE: DNA  
 : ORGANISM: synthetic  
 : FEATURE:  
 : NAME/KEY: DNA  
 : LOCATION: (1) ..(1128)  
 : : OTHER INFORMATION: pMON37402 sequence encoding permutoxin protein  
 US-10-682-011-20

Db	121	CTGCTGTACATGGATGTTAGTTATACAGAAAAAGCATGATGCGCAAGTTCTTACATGA	180
QY	181	CTGATATTATACCTTTTCTACGCTTTTCAAGCTCTGATATCGAAAAACAATTACCTCGGG	240
Db	181	CTGATATTATACCTTTTCTACGCTTTTCAAGCTCTGATATCGAAAAACAATTATCTCGGG	240
QY	241	TTCAAGAAAAATGCATTTAAACAGGCACAACCTACCTGAAAAATGATAGTCTTCTAGGCTATA	300
Db	241	TTCAAGAAAAATGCATTTAAACAGGCACAACCTACCTGAAAAATGATAGTCTTCTAGGCTATA	300
QY	301	TGGAATTAATAGTACAAAGTTGGTAAAACTTATTTGAAAGAAAACAGTTTCCGAAACAATC	360
Db	301	TGGAATTAATAGTACAAAGTTGGTAAAACTTATTTGAAAGAAAACAGTTTCCGAAACAATC	360
QY	361	CTGAAACCTATAGAGAAAGCTCTTAAAGAGTTTGGAAAAATGCTCTCTGATATGGAAGAAC	420
Db	361	CTGAAACCTATAGAGAAAGCTCTTAAAGAGTTTGGAAAAATGCTCTCTGATATGGAAGAAC	420
QY	421	TCCGAGCAAAACAAGCTTCTTATAGACACAGGACAGTTGGAGAAATGGTGAAGTCTTCTTA	480
Db	421	TCCGAGCAAAACAAGCTTCTTATAGACACAGGACAGTTGGAGAAATGGTGAAGTCTTCTTA	480
QY	481	GTATTGATGAGAGTGGAAATTAAGAGGATCAATTCGGGCTACCATTTCTGAAATTTCTTGAAG	540
Db	481	GTATTGATGAGAGTGGAAATTAAGAGGATCAATTCGGGCTACCATTTCTGAAATTTCTTGAAG	540
QY	541	GACAACTTCAGGAATATGACATTAATGCATATGCAAGACTTGGACATTTACTTTATATATGA	600
Db	541	GACAACTTCAGGAATATGACATTAATGCATATGCAAGACTTGGACATTTACTTTATATATGA	600
QY	601	TTGGAGGAACAAGATACAGAGAGTTTATTTGATGTCGTATGATPAAGATCTCCAAATGAAAAA	660
Db	601	TTGGAGGAACAAGATACAGAGAGTTTATTTGATGTCGTATGATPAAGATCTCCAAATGAAAAA	660
QY	661	ATCGAACCTTTGCTGCTGCTGCCAAGAAAAATGATACCTTTTACTTGGAAATGAGCCCTCAGA	720
Db	661	ATCGAACCTTTGCTGCTGCTGCCAAGAAAAATGATACCTTTTACTTGGAAATGAGCCCTCAGA	720
QY	721	TTTTTAAATCCTAGTGTGTCAAAATTTTAAAGCCCAAAATATGATGAGAAAAATATCTTATGCAAG	780
Db	721	TTTTTAAATCCTAGTGTGTCAAAATTTTAAAGCCCAAAATATGATGAGAAAAATATCTTATGCAAG	780
QY	781	TTCTTCAAGAAAACTTGAGAAAACTGCTGTGCATCAAGCTTTTGACAGAAATGTTGTCACT	840
Db	781	TTCTTCAAGAAAACTTGAGAAAACTGCTGTGCATCAAGCTTTTGACAGAAATGTTGTCACT	840
QY	841	CMACTTTGACATCAAAAACAAATATAGCCAGATATATTTCACTAAGTCAAAATTTAGCAACT	900
Db	841	CMACTTTGACATCAAAAACAAATATAGCCAGATATATTTCACTAAGTCAAAATTTAGCAACT	900
QY	901	CTCAGAAATGAGATGCTPAAGATGATATGACATTAAGTATTTCCACAGCAGACGCTCCACAT	960
Db	901	CTCAGAAATGAGATGCTPAAGATGATATGACATTAAGTATTTCCACAGCAGACGCTCCACAT	960
QY	961	ATTTTCCCTCCGCACTTACTTTGTTACTAATCTAGATATGAGAGAAATATAGTTCAATC	1020
Db	961	ATTTTCCCTCCGCACTTACTTTGTTACTAATCTAGATATGAGAGAAATATAGTTCAATC	1020
QY	1021	TTGTTGATGAGTGTGCTGTCTACTGCTTGTCTGATCCGGGCTTATTTATCCATTAGCGTTGCA	1080
Db	1021	TTGTTGATGAGTGTGCTGTCTACTGCTTGTCTGATCCGGGCTTATTTATCCATTAGCGTTGCA	1080
QY	1081	CGAAGCTTGCAAAAAGATTCACAGACTTTGTTCAATTAAGTATGAG	1128
Db	1081	CGAAGCTTGCAAAAAGATTCACAGACTTTGTTCAATTAAGTATGAG	1128

RESULT 4  
US-09-755-630A-258  
Sequence 258, Application US/09755630A  
Publication No. US2003019439A1  
GENERAL INFORMATION:  
APPLICANT: ALIBHAI, MURTAZA F.

```

? APPLICANT: ASTWOOD, JAMES D.
? APPLICANT: SAMPSON, HUGH A.
? APPLICANT: MOTHERTER, CHARLES A.
? TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTERINS
? FILE REFERENCE: 11899 0217 NUSO0 (MOB8217)
? CURRENT APPLICATION NUMBER: US/09/755,630A
? CURRENT FILING DATE: 2001-01-05
? PRIOR APPLICATION NUMBER: US 60/174,669
? PRIOR FILING DATE: 2000-01-06
? NUMBER OF SEQ ID NOS: 293
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 258
? LENGTH: 1128
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Synthetic construct
? US-09-755-630A-258

```

Query Match	91.9%	Score 1036.2;	DB 10;	Length 1128;
Best Local Similarity	99.2%;	Pred. No. 6.4e-25;		
Matches 1041;	Conservative	0;	Mismatches 8;	Indels 0;
			Gaps	0

[illegible]

Db	731	TGAGAAATCGTGTGATCAAGCTTTGACAGAGTTGTATCTCAAGCTTTGACATCAA	790
Qy	857	AACAAATPAGCGAATATATTCACATAGTCAAAATTTGGCAAACTCTCAGAAATTGATGC	916
Db	791	AACAAATPAGCGAATATATTCACATAGTCAAAATTTGGCAAACTCTCAGAAATTGATGC	850
Qy	917	TAAATGATGATGACATTAAGTTATTCACAGCAGCAGCTCCAAATATATTTCTCCGCATTA	976
Db	851	TAAATGATGATGACATTAAGTTATTCACAGCAGCAGCTCCAAATATATTTCTCCGCATTA	910
Qy	977	CTTGTGTAATATCTAGTATGGAAGATGGAATATGAGTTCAATCTGTGTATGGAGCTGT	1036
Db	911	CTTGTGTAATATCTAGTATGGAAGATGGAATATGAGTTCAATCTGTGTATGGAGCTGT	970
Qy	1037	TGCTACTGTGTGCTATCCGGCGTTATTTATCCATTAGCGTTGCAACGAGACTTGCACAAA	1096
Db	971	TGCTACTGTGTGCTATCCGGCGTTATTTATCCATTAGCGTTGCAACGAGACTTGCACAAA	1030
Qy	1097	GGATCCAGCAATTTGCTTCAATTAGTAAAT	1125
Db	1031	GGATCCAGCAATTTGCTTCAATTAGTAAAT	1059

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RESULT 5
US-10-658-180-258
; Sequence 258: Application US/10658180
; Publication No. US20040216187A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTENS
; FILE REFERENCE: 11899.0217.DVUS02
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US 09/755,630
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 258
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-658-180-258

Query Match          91.9%; Score 1036.2; DB 18; Length 1128;
Best Local Similarity 99.2%; Pred. No. 6.4e-253;
Matches 1041; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

    77 AGAGTGTGATTAACATATACATATACAGCAAAAGAGGACGACTACCTGACCTGCTGATCTTGAT
    |||||
    11 AGAGGCGTGAAGCTACATATACAGCAAAAGAGGACGACTACCTGACCTGCTGATCTTGAT
    |||||
    137 GTTAGTATTACAGAAATGACTGATGACGACGAAGTTCTTACATGACTGATTAATTAACCTTC
    |||||
    71 GTTAGTATTACAGAAATGACTGATGACGACGAAGTTCTTACATGACTGATTAATTAACCTTC
    |||||
    137 TACGCTTTTCAACCTCTGATTCATAAAAAACAATTTACTCAGGGTCCAGAAAAATGACATT
    |||||
    197 TACGCTTTTCAACCTCTGATTCATAAAAAACAATTTACTCAGGGTCCAGAAAAATGACATT
    |||||
    131 TACGCTTTTCAACCTCTGATTCATAAAAAACAATTTACTCAGGGTCCAGAAAAATGACATT
    |||||
    257 AACAGGACCACTACTGAAATGATGATGCTTCTGAGGCTTAATATGAAATTATTAGATACA
    |||||
    191 AACAGGACCACTACTGAAATGATGATGCTTCTGAGGCTTAATATGAAATTATTAGATACA
    |||||
    317 AGTTGGTGAACCTTAATTGAAAGAAACCAAGTTCCGAAAGACAAATCCTGAAACCTATGAGGA
    |||||
    251 AGTTGGTGAACCTTAATTGAAAGAAACCAAGTTCCGAAAGACAAATCCTGAAACCTATGAGGA
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QY 377 AGCTCTAAGAGAGTTTGCAAAATTTGCTCTGTATAGGAAGAACTCCGACAAACAAGC 436
Db 311 AGCTCTAAGAGAGTTTGCAAAATTTGCTCTGTATAGGAAGAACTCCGACAAACAAGC 370
QY 437 TTCTTATGACGACGACAGTGTGGAGAAATGTGATGCTTTCTTATGATATGATGAGGTGG 496
Db 371 TTCTTATGACGACGACAGTGTGGAGAAATGTGATGCTTTCTTATGATATGATGAGGTGG 430
QY 497 AATTAAAGGATATATCCGGCTACATCTTCGAAATTTCTTGAAGACAACTTCAGGAAT 556
Db 431 AATTAAAGGATATATCCGGCTACATCTTCGAAATTTCTTGAAGACAACTTCAGGAAT 490
QY 557 GGCAATTAATGACGATGACAGACTTGCAGATTACTTTGATGTAATGAGAGAAACAATGAC 616
Db 491 GGCAATTAATGACGATGACAGACTTGCAGATTACTTTGATGTAATGAGAGAAACAATGAC 550
QY 617 AGGAGGTTTATGATGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 676
Db 551 AGGAGGTTTATGATGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 610
QY 677 TGCCTAAGAAATGTATCTTTTACTTTCGAAATGCGCCCTCAGATTTTATCTAGTGG 736
Db 611 TGCCTAAGAAATGTATCTTTTACTTTCGAAATGCGCCCTCAGATTTTATCTAGTGG 670
QY 737 TCAAAATTTTAGGCGCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAAC 796
Db 671 TCAAAATTTTAGGCGCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAAC 730
QY 797 TGGAGAACTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 856
Db 731 TGGAGAACTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 790
QY 857 AACAAATAGCCGATATATTTCACTAAGTCAAAATTTAGCAAACTCTCCAGATTTGATGC 916
Db 791 AACAAATAGCCGATATATTTCACTAAGTCAAAATTTAGCAAACTCTCCAGATTTGATGC 850
QY 917 TAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 976
Db 851 TAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 910
QY 977 CTTTGTACTAATATAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1036
Db 911 CTTTGTACTAATATAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 970
QY 1037 TGCCTACTGTTGCTGATCCGCGTTATTTATCCATTAGCGTTGCAACGACTTGCACAAA 1096
Db 971 TGCCTACTGTTGCTGATCCGCGTTATTTATCCATTAGCGTTGCAACGACTTGCACAAA 1030
QY 1097 GGATCCAGCATTTGCTTCAATTTAGGTAAT 1125
Db 1031 GGATCCAGCATTTGCTTCAATTTAGGTCAT 1059
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RESULT 6  
US-10-682-011-26

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; Sequence 26, Application US/10682011
; GENERAL INFORMATION:
; APPLICANT: Alibhai, Murtaza
; APPLICANT: Rydel, Timothy
; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases
; FILE REFERENCE: 38-21 (51842)B
; CURRENT APPLICATION NUMBER: US/10/682,011
; PRIOR FILING DATE: 2003-10-09
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: synthetic
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FEATURE:  
; NAME/KEY: DNA  
; LOCATION: (1)-(1128)  
; OTHER INFORMATION: pMON37407 sequence encoding permuterin protein  
US-10-682-011-26

Query Match 91.9%; Score 1036.2; DB 18; Length 1128;  
Best Local Similarity 99.2%; Pred. No. 6,4e-253;  
Matches 1041; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 77 AGAGTTGATTAACATATACAGCAAAAGAGAGCTACCTGACCTGCTGATTTGAT 136
Db 11 AGAGGCTGAAGCTACATATACAGCAAAAGAGAGCTACCTGACCTGCTGATTTGAT 70
QY 137 GTTAGTTATCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 196
Db 71 GTTAGTTATCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 130
QY 197 TACTGCTTTTCAAGCTCTGATTTCAAAAACAATTAACCTGAGGTTCAAGAAAATGAT 256
Db 131 TACTGCTTTTCAAGCTCTGATTTCAAAAACAATTAACCTGAGGTTCAAGAAAATGAT 190
QY 257 AACAGCAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 316
Db 191 AACAGCAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 250
QY 317 AGTTGATGAATCTTATGAGAAACCAATTCGAGAAACAATTCGAAACCTATGAGGA 376
Db 251 AGTTGATGAATCTTATGAGAAACCAATTCGAGAAACAATTCGAAACCTATGAGGA 310
QY 377 AGCTCTAAGAGGTTTCAAAATTTGCTCTGTATAGGAAGAACTCCGACAAACAAGC 436
Db 311 AGCTCTAAGAGGTTTCAAAATTTGCTCTGTATAGGAAGAACTCCGACAAACAAGC 370
QY 437 TTCTTATGACGACGACAGTGTGGAGAAATGTGATGCTTTCTTATGATATGATGAGGTGG 496
Db 371 TTCTTATGACGACGACAGTGTGGAGAAATGTGATGCTTTCTTATGATATGATGAGGTGG 430
QY 497 AATTAAAGGATATATCCGGCTACATCTTCGAAATTTCTTGAAGACAACTTCAGGAAT 556
Db 431 AATTAAAGGATATATCCGGCTACATCTTCGAAATTTCTTGAAGACAACTTCAGGAAT 490
QY 557 GGAATTAATGACGATGACAGACTTGCAGATTACTTTGATGTAATGAGAGAAACAATGAC 616
Db 491 GGAATTAATGACGATGACAGACTTGCAGATTACTTTGATGTAATGAGAGAAACAATGAC 550
QY 617 AGGAGGTTTATGATGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 676
Db 551 AGGAGGTTTATGATGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 610
QY 677 TGCCTAAGAAATGTATCTTTTACTTTCGAAATGCGCCCTCAGATTTTATCTAGTGG 736
Db 611 TGCCTAAGAAATGTATCTTTTACTTTCGAAATGCGCCCTCAGATTTTATCTAGTGG 670
QY 737 TCAAAATTTTAGGCGCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAAC 796
Db 671 TCAAAATTTTAGGCGCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAAC 730
QY 797 TGGAGAACTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 856
Db 731 TGGAGAACTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 790
QY 857 AACAAATAGCCGATATATTTCACTAAGTCAAAATTTAGCAAACTCTCCAGATTTGATGC 916
Db 791 AACAAATAGCCGATATATTTCACTAAGTCAAAATTTAGCAAACTCTCCAGATTTGATGC 850
QY 917 TAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 976
Db 851 TAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 910
QY 977 CTTTGTACTAATATAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1036
Db 911 CTTTGTACTAATATAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 970
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Qy	1097	GGATCCAGCANTTGGCTCAATTAGATAT	1125
Db	1031	GGATCCAGCATTGCTTCATTTAGATCAT	1059

## RESULT 7

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US-09-755-630A-250
; Sequence 250, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCHERNIER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTINS
; FILE REFERENCE: 11899, 0217, NUS000 (MOB217)
; CURRENT APPLICATION NUMBER: US/09/755,630A
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 250
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-755-630A-250

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Query Match	Score	DB	Length
85.4%	963.4	10	1128

QY	24	TCATTTGAATTA	CAAAAAAATCTGTGTCTCATTAGGCACTGGCACTTACAGAGTTT	83
Db	159	TCATTTGAATTA	CAAAAAAATCTGTGTCTCATTAGGCACTGGCACTTACAGAGTTT	218
QY	84	GATTAATA	CATATACGCAAAAGGCGAGCTACCTGCACTGCTGTACATTTGATTTAGTT	143
Db	219	GATTAATA	CATATACGCAAAAGGCGAGCTACCTGCACTGCTGTACATTTGATTTAGTT	278
QY	144	ATACAGAAAA	AGACGATGAGCAAGTCTTAACATGACTGATTTTATACCTTTCTACGCT	203
Db	279	ATACAGAAAA	AGACGATGAGCAAGTCTTAACATGACTGATTTTATACCTTTCTACGCT	338
QY	204	TTTCAAGCT	CTTGGATTCAAAAAACAATTACCTCAGGGTTCAAGAAAAATGACTTAAACAGGC	263
Db	339	TTTCAAGCT	CTTGGATTCAAAAAACAATTACCTCAGGGTTCAAGAAAAATGACTTAAACAGGC	398
QY	264	ACAACTA	CTGAAATGATGATGCTTCTTGAGGCTAATATGAAATTATGTAACAAGTTGT	323
Db	399	ACAACTA	CTGAAATGATGATGCTTCTTGAGGCTAATATGAAATTATGTAACAAGTTGT	458
QY	324	GAAAACTT	ATTGAAGAAACCAAGTTTCCGAAGACAATCCTGAAACCTATGAGAAAGCTTTA	383
Db	459	GAAAACTT	ATTGAAGAAACCAAGTTTCCGAAGACAATCCTGAAACCTATGAGAAAGCTTTA	518
QY	384	AAGAGTTT	GCAAAATGCTCTCTGATTTGGAAGAAACCTCCGAGCAAAACAAGCTCTTAT	443
Db	519	AAGAGTTT	GCAAAATGCTCTCTCTGATTTGGAAGAAACCTCCGAGCAAAACAAGCTCTTAT	578
QY	444	GGAACAGGA	CAGTTGGAGAAATGGTGACTGTTCTTATATTTGATTTGAGAGTGTGAATTAGA	503
Db	579	GGAACAGGA	CAGTTGGAGAAATGGTGACTGTTCTTATATTTGATTTGAGAGTGTGAATTAGA	638
QY	504	GGATCATTT	CCGGCTACCATTTCTGAAATTTCTTGAAGACAATTCAGAAAAATGGACAAT	563

Db	639	GGGATTCATCCGGGTACCAATTCCTGCAGATTTCTTGAAAGACAACCTTCAGAAATGACAAT	698
Oy	564	AATGCAATGCAAGACTTTGGAGATTACTTTGATGCTAATTGGAGGAAACAGATACGAGGT	623
Db	699	AATGCACATGCAAGACTTGCAGATTACTTTGATGTAATTGGAGGACAAGTACGAGGT	758
Oy	624	TTATTTGACTGCTATGATTAAGTACTCTCAAAATGAAAAACAATGCACCCTTGTCTGTCCAAA	683
Db	759	TTATTTGACTGCTATGATTAAGTACTCTCAAAATGAAAAACAATGCACCCTTGTCTGTCCAAA	818
Oy	684	GAAATTGTACTCTTTTACTTTCGAAACATGCGCCCTCAGATTTTAAATCTTAGTGTCAAAAT	743
Db	819	GAAATTGTACTCTTTTACTTTCGAAACATGCGCCCTCAGATTTTAAATCTTAGTGTCAAAAT	878
Oy	744	TTAAGGCCCAAAATATGATNGAGAAATATCTTATGCAAGATTCTTCAAGAAAAAATTGGAGAA	803
Db	879	TTAAGGCCCAAAATATGATNGAGAAATATCTTATGCAAGATTCTTCAAGAAAAAATTGGAGAA	938
Oy	804	ACTGCTGTGCATCAAGCTTTTGACAGAGATTGTCATCTCAAGCTTTGACATCAAAACAAT	863
Db	939	ACTGCTGTGCATCAAGCTTTTGACAGAGATTGTCATCTCAAGCTTTGACATCAAAACAAT	998
Oy	864	AAGCCAGTAATATTCACATAAGTCAAAATTGAGCAAACTCTCAGAAATTGATGCTAAAGTG	923
Db	999	AAGCCAGTAATATTCACATAAGTCAAAATTGAGCAAACTCTCAGAAATTGATGCTAAAGTG	1058
Oy	924	TATGACATTAAGTTAATTCACAGACGAGCTTCGAAACATATATTTCTCTCGCATTAATCTTTGTT	983
Db	1059	TATGACATTAAGTTAATTCACAGACGAGCTTCGAAACATATATTTCTCTCGCATTAATCTTTGTT	1118
Oy	984	ACTAA 988	
Db	1119	ACTTA 1123	

## RESULT 8

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US-10-658-180-250
; Sequence 250, Application US/10658180
; Publication No. US20040216187A1
GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MORTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MOTHERTER, CHARLES A.
TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTENEINS
; FILE REFERENCE: 11899.0217.DVUS02
CURRENT APPLICATION NUMBER: US/10/658,180
; CURRENT FILING DATE: 2003-09-09
Prior APPLICATION NUMBER: US 09/755,630
; Prior FILING DATE: 2001-01-05
Prior APPLICATION NUMBER: US 60/174,669
; Prior FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.2
SEQ ID NO 250
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-658-180-250

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Query Match	85.4%;	Score 963.4;	DB 18;	Length 1128;
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Oy	24	TCATTTGAATTA	CAAAAAAA	TCGTGTCTC	CAATTAGCA	CTGGCACT	CACTTCA	GAGATT	83
Oy	159	TCATTTGAATTA	CAAAAAAA	TCTGTGTCT	CAATTAGCA	CTGGCACT	CACTTCA	GAGATT	218
Oy	84	GATYAAA	CATYACG	CAAAAGAG	GCAGCTA	CTTGAC	CTGCTG	TAACATTTGAT	143
Oy	219	GATYAAA	CATYATACG	CAAAAGAG	GCAGCTA	CTTGAC	CTGCTG	TAACATTTGAT	278
Oy	84	GATYAAA	CATYACG	CAAAAGAG	GCAGCTA	CTTGAC	CTGCTG	TAACATTTGAT	143
Oy	219	GATYAAA	CATYATACG	CAAAAGAG	GCAGCTA	CTTGAC	CTGCTG	TAACATTTGAT	278



QY 864 AAGCAGTATATATTCAGTCAAAATTTAGCAAACTCTCCAGAAATGATGCTAAAGATG 923  
| | | | |  
Db 999 AAGCCGATATATTCAGTCAAAATTTAGCAAACTCTCCAGAAATGATGCTAAAGATG 1058  
| | | | |  
QY 924 TATGACATAGTATTTCCAGACGAGCTCCAACTATTTTCTCCGACTTACTTTGTT 993  
| | | | |  
Db 1059 TATGACATAGTATTTCCAGACGAGCTCCAACTATTTTCTCCGACTTACTTTGTT 1118  
| | | | |  
QY 984 ACTAA 988  
| | | | |  
Db 1119 ACTTA 1123  
| | | | |  
RESULT 10  
US-09-755-630A-254  
; Sequence 254, Application US/09755630A  
; Publication No. US20030194399A1  
; GENERAL INFORMATION:  
; APPLICANT: ALIBHAI, MURTAZA F.  
; APPLICANT: ASTWOOD, JAMES D.  
; APPLICANT: SAMPERSON, HUGH A.  
; APPLICANT: MCWHERTER, CHARLES A.  
; TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTAINS  
; FILE REFERENCE: 11899.0217, NPUS00 (MOBT217)  
; CURRENT APPLICATION NUMBER: US/09/755,630A  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 60/174,669  
; NUMBER OF SEQ ID NOS: 293  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 254  
; LENGTH: 1128  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
; US-09-755-630A-254  
Query Match 80.6%; Score 909; DB 10; Length 1128;  
Best Local Similarity 100.0%; Pred. No. 1.5e-220;  
Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 24 TCATTGAATTTACAAAAAATGCTGTTGCTCTCTCATTTAGGCACTGGCACTACTTCAAGTTT 83  
| | | | |  
Db 213 TCATTGAATTTACAAAAAATGCTGTTGCTCTCTCATTTAGGCACTGGCACTACTTCAAGTTT 272  
| | | | |  
QY 84 GATPAAACATATACAGCAAAAGGCGAGCTACCTGACCTGCTGTACTTGGATGTTAGTT 143  
| | | | |  
Db 273 GATPAAACATATACAGCAAAAGGCGAGCTACCTGACCTGCTGTACTTGGATGTTAGTT 332  
| | | | |  
QY 144 ATTCAGAAATGCTGATGAGCAAGTTCTTACATGACATGATTAACCTTTCTACGCT 203  
| | | | |  
Db 333 ATTCAGAAATGCTGATGAGCAAGTTCTTACATGACATGATTAACCTTTCTACGCT 352  
| | | | |  
QY 204 TTTCAAGCTCTTGAATTTCAAAAAAATTAATCTGAGGTTCAAGAAATGATTAACAGGC 263  
| | | | |  
Db 393 TTTCAAGCTCTTGAATTTCAAAAAAATTAATCTGAGGTTCAAGAAATGATTAACAGGC 452  
| | | | |  
QY 264 ACAACTTACTGAAATGATGATGCTTCTGAGGCTTAATGGAATTTATTTAGTCAAGTTGGT 323  
| | | | |  
Db 453 ACAACTTACTGAAATGATGATGCTTCTGAGGCTTAATGGAATTTATTTAGTCAAGTTGGT 512  
| | | | |  
QY 324 GAAACTTATTTGAAAGAAACAGTTTCCGAGACAACTGAAACCTATGAGGAAGCTCTA 383  
| | | | |  
Db 513 GAAACTTATTTGAAAGAAACAGTTTCCGAGACAACTGAAACCTATGAGGAAGCTCTA 572  
| | | | |  
QY 384 AAGAGGTTTGCAGAAATTTGCTCTCTGATAGGAAGAACTCCGAGCAAAACAAGCTTCTTAT 443  
| | | | |  
Db 573 AAGAGGTTTGCAGAAATTTGCTCTCTGATAGGAAGAACTCCGAGCAAAACAAGCTTCTTAT 632  
| | | | |  
QY 444 GACCAAGACAGTTGGAGAAATGCTGCTTCTTATGATTTGATGAGGTTGAAATTAGA 503  
| | | | |

Db 633 GACACAGACAGTTGGAGAAATGCTGACTGTTCTTATGATTTGATGAGAGTGAATTAGA 692  
| | | | |  
QY 504 GGGATCATTTCCGCTACATTCATTCGAATTTCTTGAAGACAATTCAGAGAAATGACAAAT 563  
| | | | |  
Db 693 GGGATCATTTCCGCTACATTCATTCGAATTTCTTGAAGACAATTCAGAGAAATGACAAAT 752  
| | | | |  
QY 564 AATGACATGACAAAGATTTGCAAGTTACTTTGATGTAATTGGAGAAACAAGTACAGAGGT 623  
| | | | |  
Db 753 AATGACATGACAAAGATTTGCAAGTTACTTTGATGTAATTGGAGAAACAAGTACAGAGGT 812  
| | | | |  
QY 624 TTATTGACTGCTATGATTAAGTACTCCAAATGAAAACAATGACACCTTTGCTGTCGCAAA 683  
| | | | |  
Db 813 TTATTGACTGCTATGATTAAGTACTCCAAATGAAAACAATGACACCTTTGCTGTCGCAAA 872  
| | | | |  
QY 684 GAAATTTGACTTTTACTTTCGAACATGAGCCCTCAGATTTTAAATCTAGTGTCAAAAT 743  
| | | | |  
Db 873 GAAATTTGACTTTTACTTTCGAACATGAGCCCTCAGATTTTAAATCTAGTGTCAAAAT 922  
| | | | |  
QY 744 TTAGSCCCAAATATGATGAAATATCTTATGCAAGTTCTTCAAGAAAACCTTGGAGAA 803  
| | | | |  
Db 933 TTAGSCCCAAATATGATGAAATATCTTATGCAAGTTCTTCAAGAAAACCTTGGAGAA 992  
| | | | |  
QY 804 ACTCGTGCATCAAGCTTTGACAGAGTTGTCATCTCAAGCTTTGACATCAAAACAAT 863  
| | | | |  
Db 993 ACTCGTGCATCAAGCTTTGACAGAGTTGTCATCTCAAGCTTTGACATCAAAACAAT 1052  
| | | | |  
QY 864 AAGCAGTATATATTCAGTCAAAATTTAGCAAACTCTCCAGAAATGATGCTAAAGATG 923  
| | | | |  
Db 1053 AAGCCGATATATTCAGTCAAAATTTAGCAAACTCTCCAGAAATGATGCTAAAGATG 1112  
| | | | |  
QY 924 TATGACATA 932  
| | | | |  
Db 1113 TATGACATA 1121  
| | | | |  
RESULT 11  
US-10-658-180-254  
; Sequence 254, Application US/10658180  
; Publication No. US20040216187A1  
; GENERAL INFORMATION:  
; APPLICANT: ALIBHAI, MURTAZA F.  
; APPLICANT: ASTWOOD, JAMES D.  
; APPLICANT: SAMPERSON, HUGH A.  
; APPLICANT: MCWHERTER, CHARLES A.  
; TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTAINS  
; FILE REFERENCE: 11899.0217, DVS02  
; CURRENT APPLICATION NUMBER: US/10/658,180  
; PRIOR FILING DATE: 2003-09-09  
; PRIOR APPLICATION NUMBER: US 09/755,630  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 60/174,669  
; NUMBER OF SEQ ID NOS: 295  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 254  
; LENGTH: 1128  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
; US-10-658-180-254  
Query Match 80.6%; Score 909; DB 18; Length 1128;  
Best Local Similarity 100.0%; Pred. No. 1.5e-220;  
Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 24 TCATTGAATTTACAAAAAATGCTGTTGCTCTCTCATTTAGGCACTGGCACTACTTCAAGTTT 83  
| | | | |  
Db 213 TCATTGAATTTACAAAAAATGCTGTTGCTCTCTCATTTAGGCACTGGCACTACTTCAAGTTT 272  
| | | | |  
QY 84 GATPAAACATATACAGCAAAAGGCGAGCTACCTGACCTGCTGTACTTGGATGTTAGTT 143  
| | | | |  
Db 273 GATPAAACATATACAGCAAAAGGCGAGCTACCTGACCTGCTGTACTTGGATGTTAGTT 332  
| | | | |

QY	144	ATACAGAAATGACTGATGACGAGAGTCTTAACAATGACTGATTTATCTTCTAAGTCT	203
Db	333	ATACAGAAATGACTGATGACGAGAGTCTTAACAATGACTGATTTATCTTCTAAGTCT	392
QY	204	TTTCAAGCTCTTGATGAAAAAACAATTACCTCAGGGTTCAAGAAATGACTTAAAGGC	263
Db	393	TTTCAAGCTCTTGATGAAAAAACAATTACCTCAGGGTTCAAGAAATGACTTAAAGGC	452
QY	264	ACAACTACTGAATGATGATGCTTCTGAGGCTAATATGAAATTTATGTAACAAGTGGT	323
Db	453	ACAACTACTGAATGATGATGCTTCTGAGGCTAATATGAAATTTATGTAACAAGTGGT	512
QY	324	GAAACCTTATTTGAAGAAACCGATTTCCGAACAATCCGTAAACCTATGAGAAAGCTGTA	383
Db	513	GAAACCTTATTTGAAGAAACCGATTTCCGAACAATCCGTAAACCTATGAGAAAGCTGTA	572
QY	384	AAGAGTTTGGCAAAATTCCTCTGATGAGAAACCTCCAGCAACCAAGCTTCTTAT	443
Db	573	AAGAGTTTGGCAAAATTCCTCTGATGAGAAACCTCCAGCAACCAAGCTTCTTAT	632
QY	444	GGACCAAGACAGTTGGAGAAATGTGACTGTTCTTAGTATTTGATGAGAGTGAATTGA	503
Db	633	GGACCAAGACAGTTGGAGAAATGTGACTGTTCTTAGTATTTGATGAGAGTGAATTGA	692
QY	504	GGGATCAATCCGGGCTACCATCTCGAATTTCTGAAAGACAACCTCAGAAATGGACAT	563
Db	693	GGGATCAATCCGGGCTACCATCTCGAATTTCTGAAAGACAACCTCAGAAATGGACAT	752
QY	564	AATCAGATGCAGACTTCGCAGATTACTTTGATGTAATTGAGAGAACAAATGACAGAGT	623
Db	753	AATCAGATGCAGACTTCGCAGATTACTTTGATGTAATTGAGAGAACAAATGACAGAGT	812
QY	624	TTATTGACTGCTATGATTAATGTAATCTCAATGAAACCAATGCAACCTTGTCTGCTCAA	683
Db	813	TTATTGACTGCTATGATTAATGTAATCTCAATGAAACCAATGCAACCTTGTCTGCTCAA	872
QY	684	GAAATGACCTTTTCTTCTGAAATGAGGCTCGATTTTAAATCCATGAGTCAAAAT	743
Db	873	GAAATGACCTTTTCTTCTGAAATGAGGCTCGATTTTAAATCCATGAGTCAAAAT	932
QY	744	TTAGGCCCAAAATATGATGAAAAATATCTTATGCAAGTCTTCAAGAAAACTTGGAGA	803
Db	933	TTAGGCCCAAAATATGATGAAAAATATCTTATGCAAGTCTTCAAGAAAACTTGGAGA	992
QY	804	ACTGTGTGCATCAAGCTTTGACAGAAATGTGATCTCAAGCTTTGACATCAAAACAAT	863
Db	993	ACTGTGTGCATCAAGCTTTGACAGAAATGTGATCTCAAGCTTTGACATCAAAACAAT	1052
QY	864	AAGCAGTAATTTCACTTAAGTCAAAATTTAGCAAACTCCAGAAATTTGATGCTTAAGT	923
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QY	924	TATGACATA 932	
Db	1113	TATGACATA 1121	
RESULT 12			
US-10-682-011-24			
: Sequence 24, Application US/10682011			
: Publication No. US20040253699A1			
: GENERAL INFORMATION:			
: APPLICANT: Alibhai, Murtaza			
: TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases			
: FILE REFERENCE: 38-21 (51842)B			
: CURRENT FILING DATE: 2003-10-09			
: PRIOR APPLICATION NUMBER: US/09/755,274			
: NUMBER OF SEQ ID NOS: 60			
: SOFTWARE: SeqId version 3.0			

[illegible]









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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: April 8, 2005, 07:18:52 ; Search time 175 Seconds  
(without alignments)  
808.882 Million cell updates/sec

Title: US-10-658-180-247

Perfect score: 1865

Sequence: 1 SLNYKKMLILSLGTSTSEF.....LSISVATRLAKQDPAPASIR 366

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1980s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1865	100.0	366	4 AAG99308	AAG99308 Permutin
2	1865	100.0	366	8 ADM93060	ADM93060 Permutin
3	1865	100.0	389	4 AAG99314	AAG99314 Permutin
4	1865	100.0	389	8 ADM93072	ADM93072 Permutin
5	1769	94.9	389	4 AAG99315	AAG99315 Permutin
6	1769	94.9	389	8 ADM93074	ADM93074 Permutin
7	1753	94.0	366	4 AAG99311	AAG99311 Permutin
8	1753	94.0	366	8 ADM93066	ADM93066 Permutin
9	1645	88.2	366	4 AAG99309	AAG99309 Permutin
10	1645	88.2	366	8 ADM93062	ADM93062 Permutin
11	1544	82.8	366	4 AAG99310	AAG99310 Permutin
12	1544	82.8	366	8 ADM93064	ADM93064 Permutin
13	1480	79.4	366	4 AAG99312	AAG99312 Permutin
14	1480	79.4	366	8 ADM93068	ADM93068 Permutin
15	1139	61.1	367	4 AAG99081	AAG99081 Pre-cleav
16	1139	61.1	367	8 ADM93080	ADM93080 Post-cleav
17	1139	61.1	386	4 AAG99325	AAG99325 Patatin h
18	1139	61.1	386	4 AAG99313	AAG99313 Permutin
19	1139	61.1	386	4 AAG99079	AAG99079 Potato pa
20	1139	61.1	386	8 ADM93070	ADM93070 Permutin
21	1139	61.1	386	8 ADM93040	ADM93040 Heartleaf
22	1139	61.1	386	8 ADM93078	ADM93078 Potato pa
23	1139	61.1	452	8 AAG99080	AAG99080 Pre-cleav
24	1139	61.1	452	8 ADM93079	ADM93079 Pre-cleav
25	1030.5	55.3	383	2 AAR72790	AAR72790 Patatin c

26	1030.5	55.3	383	2 AAW74512	AAW74512 Amino aci
27	1019	54.6	386	4 AAG99319	AAG99319 Patatin i
28	1019	54.6	386	8 ADM93045	ADM93045 Patatin i
29	1017	54.5	386	4 AAG99318	AAG99318 Patatin i
30	1017	54.5	386	8 ADM93044	ADM93044 Patatin i
31	1014	54.4	380	2 AAR72789	AAR72789 Patatin c
32	1014	54.4	381	2 AAW74511	AAW74511 Amino aci
33	1014	54.4	386	4 AAG99322	AAG99322 Patatin i
34	1014	54.4	386	8 ADM93043	ADM93043 Patatin i
35	1013	54.3	364	4 AAG99321	AAG99321 Patatin i
36	1013	54.3	364	8 ADM93042	ADM93042 Patatin i
37	1001.5	53.7	365	4 AAG99320	AAG99320 Patatin i
38	1001.5	53.7	365	8 ADM93041	ADM93041 Patatin i
39	618.5	33.2	400	3 AAG20550	AAG20550 Arabidops
40	618.5	33.2	400	3 AAG50025	AAG50025 Arabidops
41	614	32.9	383	3 AAG50026	AAG50026 Arabidops
42	614	32.9	383	3 AAG20551	AAG20551 Arabidops
43	614	32.9	414	3 AAG30649	AAG30649 Arabidops
44	613	32.9	420	5 AAM52549	AAM52549 Nicotiana
45	609.5	32.7	405	4 AAE02385	AAE02385 Rice lipi

## ALIGNMENTS

## RESULT 1

AAAG99308 standard; protein; 366 AA.

AAAG99308;

28-SEP-2001 (first entry)

Permutin protein #1.

Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;

larva growth; lipid acyl hydrolase; insecticide.

Unidentified.

WO200149834-A2.

12-JUL-2001.

05-JAN-2001; 2001WO-US000342.

06-JAN-2000; 2000US-0174669P.

(MONS ) MONSANTO CO.

Alibhai MF, Astwood JD, McWhorter CA, Sampson HA;

WPI; 2001-441874/47.

Modified potato patatin proteins with reduced antigenicity, useful as insecticides for controlling e.g. round worm and root worm.

Claim 26; Page 183-184; 223pp; English.

The present invention relates to modified potato patatins that maintain enzymatic and insecticidal activity but which have reduced allergenicity. Groups (especially Tyr) which bind to anti-patatin antibodies were identified and glycosylation sites involved in antibody binding were removed via site directed mutagenesis. The patatins stunt the growth of larvae so that maturation is prevented or delayed. The patatins also have non-specific lipid acyl hydrolase activity. The modified patatins are also useful for inhibiting the activity of corn round worms.

Dellargenised protein can be used as insecticides, as nutritional supplements and as immunising agents. The present sequence was used to illustrate the present invention

Sequence 366 AA;

XX

Query Match 100.0%; Score 1865; DB 4; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-163;  
 Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC of a plant or plant part, for controlling insects (e.g. corn rootworm),  
 CC as nutritional supplements, and in immunotherapy protocols. The present  
 CC sequence represents the amino acid sequence of permutein.

XX Sequence 366 AA;

Query Match 100.0%; Score 1865; DB 8; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-163;  
 Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC of a plant or plant part, for controlling insects (e.g. corn rootworm),  
 CC as nutritional supplements, and in immunotherapy protocols. The present  
 CC sequence represents the amino acid sequence of permutein.

XX Sequence 366 AA;

RESULT 2  
 ID ADM93060 standard; protein: 366 AA.

AC ADM93060;  
 DT 03-JUN-2004 (first entry)  
 DE Permuterin protein #1.  
 KM lipid acyl hydrolase; corn rootworm; insect infestation; plant;  
 KM insect control; nutritional supplement; ds; permutein.  
 OS Synthetic.  
 PN US6657046-B1.  
 PD 02-DEC-2003.  
 PF 05-JAN-2001; 2001US-00755274.  
 PR 06-JAN-2000; 2000US-0174669P.  
 PR 21-JUL-2000; 2000US-0219912P.  
 PA (MONS ) MONSANTO TECHNOLOGY LLC.  
 PI Alibhai MF, Rydel TJ;  
 DR WPI; 2004-058368/06.  
 DR N-PSDB; ADM93059.

PT New lipid acyl hydrolase proteins, useful for inhibiting insect  
 PT infestation of a plant or plant part, for controlling insects, as  
 PT nutritional supplements, or in immunotherapy protocols.

PS Example 6; SEQ ID NO 21; 73pp; English.

CC The invention relates to an isolated peptide exhibiting lipid acyl  
 CC hydrolase activity and corn rootworm insect inhibitory bioactivity. The  
 CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation

Query Match 100.0%; Score 1865; DB 8; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-163;  
 Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC of a plant or plant part, for controlling insects (e.g. corn rootworm),  
 CC as nutritional supplements, and in immunotherapy protocols. The present  
 CC sequence represents the amino acid sequence of permutein.

XX Sequence 366 AA;

Query Match 100.0%; Score 1865; DB 8; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-163;  
 Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC of a plant or plant part, for controlling insects (e.g. corn rootworm),  
 CC as nutritional supplements, and in immunotherapy protocols. The present  
 CC sequence represents the amino acid sequence of permutein.

XX Sequence 366 AA;

RESULT 3  
 ID AAG99314 standard; protein: 389 AA.

AC AAG99314;  
 DT 28-SEP-2001 (first entry)  
 DE Permuterin protein #7.  
 KM Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;  
 KM larva growth; lipid acyl hydrolase; insecticide.  
 OS Unidentified.  
 PN WO200149834-A2.  
 PD 12-JUL-2001.  
 PF 05-JAN-2001; 2001WO-US000342.  
 PR 06-JAN-2000; 2000US-0174669P.  
 PA (MONS ) MONSANTO CO.  
 PI Alibhai MF, Actwood JD, Mcwhorter CA, Sampson HA;  
 DR WPI; 2001-441874/47.

PT Modified potato patatin proteins with reduced antigenicity, useful as  
 PT insecticides for controlling e.g. round worm and root worm.

PS Claim 60; Page 198-199; 223pp; English.

XX

CC The present invention relates to modified potato patatins that maintain  
CC enzymatic and insecticidal activity but which have reduced allergenicity.  
CC Groups (especially Tyr) which bind to anti-patatin antibodies were  
CC identified and glycosylation sites involved in antibody binding were  
CC removed via site directed mutagenesis. The patatins stunt the growth of  
CC larvae so that maturation is prevented or delayed. The patatins also have  
CC non-specific lipid acyl hydrolase activity. The modified patatins are  
CC also useful for inhibiting the activity of corn root worms.  
CC Deallergensd protein can be used as insecticides, as nutritional  
CC supplements and as immunising agents. The present sequence was used to  
CC illustrate the present invention

CC  
XX  
SQ Sequence 389 AA;

Query Match 100.0%; Score 1865; DB 4; Length 389;  
Best Local Similarity 100.0%; Pred. No.7.5e-163;  
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSLGTGTTSEFDKTYTAKEATWTAVHMLVYIOKMTDAASSYMTDYVYSTA 60  
DB 24 SLNYKKMLLSLGTGTTSEFDKTYTAKEATWTAVHMLVYIOKMTDAASSYMTDYVYSTA 83  
QY 61 FOALDSKNNYLRVOENALTGTTTMDASANNELLVOGENTLKKPVSDNPETYEAL 120  
DB 84 FOALDSKNNYLRVOENALTGTTTMDASANNELLVOGENTLKKPVSDNPETYEAL 143  
QY 121 KRPAKLISDRKKLRANKASYGPOLGEMTVLSIDGGIRGIIIPATLLEFLBQLOEMDN 180  
DB 144 KRPAKLISDRKKLRANKASYGPOLGEMTVLSIDGGIRGIIIPATLLEFLBQLOEMDN 203  
QY 181 NADARLADYFDVIGTSTGILTMAMISTPENNRPFPAAKEIVPFYEHGPOIFNPSGOI 240  
DB 204 NADARLADYFDVIGTSTGILTMAMISTPENNRPFPAAKEIVPFYEHGPOIFNPSGOI 263  
QY 241 LGRKYDGKYMQLVQEKLGSTRVHQAITEVVISFDIKTKNPVIFTKSNLANSPELDAM 300  
DB 264 LGRKYDGKYMQLVQEKLGSTRVHQAITEVVISFDIKTKNPVIFTKSNLANSPELDAM 323  
QY 301 YDISYSTAAAPTYPPHYFVTNTSNGDEVEFNLDGAVATVADPALISVATRLAQKP 360  
DB 324 YDISYSTAAAPTYPPHYFVTNTSNGDEVEFNLDGAVATVADPALISVATRLAQKP 383  
QY 361 AFASIR 366  
DB 384 AFASIR 389

RESULT 4

ADM93072 standard; protein; 389 AA.

ADM93072;

03-JUN-2004 (first entry)

Permutin protein #7.

lipid acyl hydrolase; corn rootworm; insect infestation; plant;  
insect control; nutritional supplement; ds; permutin.

Synthetic.

US6657046-B1.

02-DEC-2003.

05-JAN-2001; 2001US-00755274.

06-JAN-2000; 2000US-0174669P.

21-JUL-2000; 2000US-0219912P.

(MONS ) MONSANTO TECHNOLOGY LLC.

PI Aibhai MF, Rydel TJ;  
XX WPI; 2004-056368/06.  
DR N-PSDB; ADM93071.  
XX  
PT New lipid acyl hydrolase proteins, useful for inhibiting insect  
infestation of a plant or plant part, for controlling insects, as  
nutritional supplements, or in immunotherapy protocols.  
XX  
PS Example 6; SEQ ID NO 33; 73pp; English.

XX  
XX The invention relates to an isolated peptide exhibiting lipid acyl  
hydrolase activity and corn rootworm insect inhibitory bioactivity. The  
lipid acyl hydrolase peptide is useful for inhibiting insect infestation  
of a plant or plant part, for controlling insects (e.g. corn rootworm),  
as nutritional supplements, and in immunotherapy protocols. The present  
sequence represents the amino acid sequence of permutin.

CC  
XX  
SQ Sequence 389 AA;

Query Match 100.0%; Score 1865; DB 8; Length 389;  
Best Local Similarity 100.0%; Pred. No.7.5e-163;  
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSLGTGTTSEFDKTYTAKEATWTAVHMLVYIOKMTDAASSYMTDYVYSTA 60  
DB 24 SLNYKKMLLSLGTGTTSEFDKTYTAKEATWTAVHMLVYIOKMTDAASSYMTDYVYSTA 83  
QY 61 FOALDSKNNYLRVOENALTGTTTMDASANNELLVOGENTLKKPVSDNPETYEAL 120  
DB 84 FOALDSKNNYLRVOENALTGTTTMDASANNELLVOGENTLKKPVSDNPETYEAL 143  
QY 121 KRPAKLISDRKKLRANKASYGPOLGEMTVLSIDGGIRGIIIPATLLEFLBQLOEMDN 180  
DB 144 KRPAKLISDRKKLRANKASYGPOLGEMTVLSIDGGIRGIIIPATLLEFLBQLOEMDN 203  
QY 181 NADARLADYFDVIGTSTGILTMAMISTPENNRPFPAAKEIVPFYEHGPOIFNPSGOI 240  
DB 204 NADARLADYFDVIGTSTGILTMAMISTPENNRPFPAAKEIVPFYEHGPOIFNPSGOI 263  
QY 241 LGRKYDGKYMQLVQEKLGSTRVHQAITEVVISFDIKTKNPVIFTKSNLANSPELDAM 300  
DB 264 LGRKYDGKYMQLVQEKLGSTRVHQAITEVVISFDIKTKNPVIFTKSNLANSPELDAM 323  
QY 301 YDISYSTAAAPTYPPHYFVTNTSNGDEVEFNLDGAVATVADPALISVATRLAQKP 360  
DB 324 YDISYSTAAAPTYPPHYFVTNTSNGDEVEFNLDGAVATVADPALISVATRLAQKP 383  
QY 361 AFASIR 366  
DB 384 AFASIR 389

RESULT 5

AAG99315 standard; protein; 389 AA.

AAG99315;

28-SEP-2001 (first entry)

Permutin protein #8.

Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;  
larva growth; lipid acyl hydrolase; insecticide.

Unidentified.

WO200149834-A2.

12-JUL-2001.

05-JAN-2001; 2001WO-US000342.



XX MO200149834-A2.  
PN 12-JUL-2001.  
XX 05-JAN-2001; 2001WO-US000342.  
XX 06-JAN-2000; 2000US-0174669P.  
XX (MONS ) MONSANTO CO.  
XX Alibhai MF, Astwood JD, Mcwherter CA, Sampson HA;  
XX MPI; 2001-441874/47.  
XX Modified potato patatin proteins with reduced antigenicity, useful as  
PT insecticides for controlling e.g. round worm and root worm.  
XX  
XX Claim 27; Page 190-192; 223pp; English.  
XX  
XX The present invention relates to modified potato patatins that maintain  
CC enzymatic and insecticidal activity but which have reduced allergenicity.  
CC Groups (especially Tyr) which bind to anti-patatin antibodies were  
CC identified and glycosylation sites involved in antibody binding were  
CC removed via site directed mutagenesis. The patatins stunt the growth of  
CC larvae so that maturation is prevented or delayed. The patatins also have  
CC non-specific lipid acyl hydrolase activity. The modified patatins are  
CC also useful for inhibiting the activity of corn root worms.  
CC Dehydrated protein can be used as insecticides, as nutritional  
CC supplements and as immunising agents. The present sequence was used to  
CC illustrate the present invention  
XX  
XX Sequence 366 AA;

Query Match 94.0%; Score 1753; DB 4; Length 366;  
Best Local Similarity 99.7%; Pred. No. 1.4e-152;  
Matches 343; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 TTTAKAAATWTAHMMVLVIQKMTDAASVWTDYLLSTAFOALDSKNNYLKVGENALTGTT 82  
DB 1 TTTAKAAATWTAHMMVLVIQKMTDAASVWTDYLLSTAFOALDSKNNYLKVGENALTGTT 60  
QY 83 TEMDDASEANMELLVQGENLKKPVSEDPETYEALKKRFALDSRKKLRANKASYGP 142  
DB 61 TEMDDASEANMELLVQGENLKKPVSEDPETYEALKKRFALDSRKKLRANKASYGP 120  
QY 143 GOLGEWTVLSTIDGGIRGIIIPATILEFLEGOLOEMDNNDARLADYFDVIGSTGGL 202  
DB 121 GOLGEWTVLSTIDGGIRGIIIPATILEFLEGOLOEMDNNDARLADYFDVIGSTGGL 180  
QY 203 TAMISTPNENNRPPAAKEIVPFYFEHGPQIFNPSCQILGPKYDGKYLQVLOEKLGETR 262  
DB 181 TAMISTPNENNRPPAAKEIVPFYFEHGPQIFNPSCQILGPKYDGKYLQVLOEKLGETR 240  
QY 263 VHQALTEVVISSEDITKNKPVITKSNLANSPELDKMDISYSTAAAPYFPHPHYVTN 322  
DB 241 VHQALTEVVISSEDITKNKPVITKSNLANSPELDKMDISYSTAAAPYFPHPHYVTN 300  
QY 323 TSNGDEYEFNLVDGAATVADPALLSISVATRLAQODPAFASIR 366  
DB 301 TSNGDEYEFNLVDGAATVADPALLSISVATRLAQODPAFASIR 344

RESULT 8  
ADM93066  
ID ADM93066 standard; protein; 366 AA.  
XX  
XX ADM93066;  
XX  
XX 03-JUN-2004 (first entry)  
XX  
XX Permutectin protein #4.  
XX

KM lipid acyl hydrolase; corn rootworm; insect infestation; plant;  
KM insect control; nutritional supplement; de; permutectin.  
XX  
XX Synthetic.  
XX  
XX US6657046-B1.  
XX  
XX  
XX 02-DEC-2003.  
XX  
XX  
XX 05-JAN-2001; 2001US-00755274.  
XX  
XX 06-JAN-2000; 2000US-0174669P.  
XX 21-JUL-2000; 2000US-0219912P.  
XX  
XX (MONS ) MONSANTO TECHNOLOGY LLC.  
XX  
XX Alibhai MF, Rydel TJ;  
XX MPI; 2004-058368/06.  
XX N-PSDB; ADM93065.  
XX  
XX  
XX New lipid acyl hydrolase proteins, useful for inhibiting insect  
PT infestation of a plant or plant part, for controlling insects, as  
PT nutritional supplements, or in immunotherapy protocols.  
XX  
XX  
XX Example 6; SEQ ID NO 27; 73pp; English.  
XX  
XX The invention relates to an isolated peptide exhibiting lipid acyl  
CC hydrolase activity and corn rootworm insect inhibitory bioactivity. The  
CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation  
CC of a plant or plant part, for controlling insects (e.g. corn rootworm),  
CC as nutritional supplements, and in immunotherapy protocols. The present  
CC sequence represents the amino acid sequence of permutectin.  
XX  
XX Sequence 366 AA;

Query Match 94.0%; Score 1753; DB 8; Length 366;  
Best Local Similarity 99.7%; Pred. No. 1.4e-152;  
Matches 343; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 TTTAKAAATWTAHMMVLVIQKMTDAASVWTDYLLSTAFOALDSKNNYLKVGENALTGTT 82  
DB 1 TTTAKAAATWTAHMMVLVIQKMTDAASVWTDYLLSTAFOALDSKNNYLKVGENALTGTT 60  
QY 83 TEMDDASEANMELLVQGENLKKPVSEDPETYEALKKRFALDSRKKLRANKASYGP 142  
DB 61 TEMDDASEANMELLVQGENLKKPVSEDPETYEALKKRFALDSRKKLRANKASYGP 120  
QY 143 GOLGEWTVLSTIDGGIRGIIIPATILEFLEGOLOEMDNNDARLADYFDVIGSTGGL 202  
DB 121 GOLGEWTVLSTIDGGIRGIIIPATILEFLEGOLOEMDNNDARLADYFDVIGSTGGL 180  
QY 203 TAMISTPNENNRPPAAKEIVPFYFEHGPQIFNPSCQILGPKYDGKYLQVLOEKLGETR 262  
DB 181 TAMISTPNENNRPPAAKEIVPFYFEHGPQIFNPSCQILGPKYDGKYLQVLOEKLGETR 240  
QY 263 VHQALTEVVISSEDITKNKPVITKSNLANSPELDKMDISYSTAAAPYFPHPHYVTN 322  
DB 241 VHQALTEVVISSEDITKNKPVITKSNLANSPELDKMDISYSTAAAPYFPHPHYVTN 300  
QY 323 TSNGDEYEFNLVDGAATVADPALLSISVATRLAQODPAFASIR 366  
DB 301 TSNGDEYEFNLVDGAATVADPALLSISVATRLAQODPAFASIR 344

RESULT 9  
AAG9309  
ID AAG9309 standard; protein; 366 AA.  
XX  
XX AAG9309;  
XX  
XX 28-SEP-2001 (first entry)  
XX

DE Permutin protein #2.  
XX Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;  
KW larva growth; lipid acyl hydrolase; insecticide.  
XX Unidentified.  
OS  
PN WO200149834-A2.  
XX  
XX 12-JUL-2001.  
XX  
XX 05-JAN-2001; 2001MO-US000342.  
XX  
XX 06-JAN-2000; 2000US-0174669P.  
XX  
XX (MONS ) MONSANTO CO.  
XX  
XX Alibhai MF, Astwood JD, McWherter CA, Sampson HA;  
XX WPI; 2001-441874/47.  
XX  
XX Modified potato patatin proteins with reduced antigenicity, useful as  
XX insecticides for controlling e.g. round worm and root worm.  
XX  
XX Claim 60; Page 186-187; 223pp; English.  
XX  
XX The present invention relates to modified potato patatins that maintain  
XX enzymatic and insecticidal activity but which have reduced allergenicity.  
XX Groups (especially Tyr) which bind to anti-patatin antibodies were  
XX identified and glycosylation sites involved in antibody binding were  
XX removed via site directed mutagenesis. The patatins stunt the growth of  
XX larvae so that maturation is prevented or delayed. The patatins also have  
XX non-specific lipid acyl hydrolase activity. The modified patatins are  
XX also useful for inhibiting the activity of corn round worms.  
XX Deallerenssed protein can be used as insecticides, as nutritional  
XX supplements and as immunising agents. The present sequence was used to  
XX illustrate the present invention  
XX  
XX Sequence 366 AA;  
SQ

Query Match 88.2%; Score 1645; DB 4; Length 366;  
Best Local Similarity 100.0%; Pred. No. 1.3e-142;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKMLLSLGTGTTSEFDKTYTAKEATWTAHVHMLVIOKMTDAASSYMTDYLLSTA 60  
DB 46 SLNYKMLLSLGTGTTSEFDKTYTAKEATWTAHVHMLVIOKMTDAASSYMTDYLLSTA 105  
QY 61 FQALDSKNNYLKRVQENALTGTTTMDASBANMELLVQVGENLLKKPVSEDNPEYEEAL 120  
DB 106 FQALDSKNNYLKRVQENALTGTTTMDASBANMELLVQVGENLLKKPVSEDNPEYEEAL 165  
QY 121 KRPALKLSRKKLRANKASVGPQLGEMTVLSIDGGIRGIIIPATILFLEBQLOEMDN 180  
DB 166 KRPALKLSRKKLRANKASVGPQLGEMTVLSIDGGIRGIIIPATILFLEBQLOEMDN 225  
QY 181 NADARLADYFDVIGSTGGLLTAMISTPENNNRPPAAKEIIVPFYFEGHPOIFNPSGOI 240  
DB 226 NADARLADYFDVIGSTGGLLTAMISTPENNNRPPAAKEIIVPFYFEGHPOIFNPSGOI 285  
QY 241 LGPKYDGKTLMOVLQEKLGSTRVHQALTEVVISFDIKTNKPVIFTKSNLANSPELDAM 300  
DB 286 LGPKYDGKTLMOVLQEKLGSTRVHQALTEVVISFDIKTNKPVIFTKSNLANSPELDAM 345  
QY 301 YDISYSTAAAPTYFPPHYFVT 321  
DB 346 YDISYSTAAAPTYFPPHYFVT 366

RESULT 10  
ADM93062  
ID ADM93062 standard; protein; 366 AA.  
XX

AC ADM93062;  
XX  
XX 03-JUN-2004 (first entry)  
XX  
XX Permutin protein #2.  
DE  
XX  
XX  
XX lipid acyl hydrolase; corn rootworm; insect infestation; plant;  
KW insect control; nutritional supplement; ds; permutin.  
XX  
XX Synthetic.  
OS  
XX  
XX US6657046-B1.  
XX  
XX 02-DEC-2003.  
XX  
XX 05-JAN-2001; 2001US-00755274.  
XX  
XX 06-JAN-2000; 2000US-0174669P.  
XX  
XX 21-JUL-2000; 2000US-0219912P.  
XX  
XX (MONS ) MONSANTO TECHNOLOGY LLC.  
XX  
XX Alibhai MF, Rydel TJ;  
XX  
XX WPI; 2004-058368/06.  
XX  
XX N-PSDB; ADM93061.  
XX  
XX New lipid acyl hydrolase proteins, useful for inhibiting insect  
XX infestation of a plant or plant part, for controlling insects, as  
XX nutritional supplements, or in immunotherapy protocols.  
XX  
XX Example 6; SEQ ID NO 23; 73pp; English.  
XX  
XX The invention relates to an isolated peptide exhibiting lipid acyl  
XX hydrolase activity and corn rootworm insect inhibitory bioactivity. The  
XX lipid acyl hydrolase peptide is useful for inhibiting insect infestation  
XX of a plant or plant part, for controlling insects (e.g. corn rootworm),  
XX as nutritional supplements, and in immunotherapy protocols. The present  
XX sequence represents the amino acid sequence of permutin.  
XX  
XX Sequence 366 AA;  
SQ

Query Match 88.2%; Score 1645; DB 8; Length 366;  
Best Local Similarity 100.0%; Pred. No. 1.3e-142;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKMLLSLGTGTTSEFDKTYTAKEATWTAHVHMLVIOKMTDAASSYMTDYLLSTA 60  
DB 46 SLNYKMLLSLGTGTTSEFDKTYTAKEATWTAHVHMLVIOKMTDAASSYMTDYLLSTA 105  
QY 61 FQALDSKNNYLKRVQENALTGTTTMDASBANMELLVQVGENLLKKPVSEDNPEYEEAL 120  
DB 106 FQALDSKNNYLKRVQENALTGTTTMDASBANMELLVQVGENLLKKPVSEDNPEYEEAL 165  
QY 121 KRPALKLSRKKLRANKASVGPQLGEMTVLSIDGGIRGIIIPATILFLEBQLOEMDN 180  
DB 166 KRPALKLSRKKLRANKASVGPQLGEMTVLSIDGGIRGIIIPATILFLEBQLOEMDN 225  
QY 181 NADARLADYFDVIGSTGGLLTAMISTPENNNRPPAAKEIIVPFYFEGHPOIFNPSGOI 240  
DB 226 NADARLADYFDVIGSTGGLLTAMISTPENNNRPPAAKEIIVPFYFEGHPOIFNPSGOI 285  
QY 241 LGPKYDGKTLMOVLQEKLGSTRVHQALTEVVISFDIKTNKPVIFTKSNLANSPELDAM 300  
DB 286 LGPKYDGKTLMOVLQEKLGSTRVHQALTEVVISFDIKTNKPVIFTKSNLANSPELDAM 345  
QY 301 YDISYSTAAAPTYFPPHYFVT 321  
DB 346 YDISYSTAAAPTYFPPHYFVT 366

RESULT 11  
AAG9310



ID	AA699310 standard; protein; 366 AA.
XX	
AC	AAG99310;
DT	28-SEP-2001 (first entry)
DE	Permuterin protein #3.
XX	
KM	Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;
KW	larva growth; lipid acyl hydrolase; insecticide.
XX	
OS	Unidentified.
XX	
PN	MO200149834-AZ:
XX	
PD	12-JUL-2001.
XX	
PJ	05-JAN-2001; 2001MO-US000342.
PF	
XX	06-JAN-2000; 2000US-0174669P.
ER	
XX	(MONS ) MONSANTO CO.
PA	
PI	Alibhai MF, Astwood JD, Mcwherter CA, Sampson HA;
XX	
XX	WPI; 2001-441874/47.
DR	
XX	
PT	Modified potato patatin proteins with reduced antigenicity, useful as
PT	insecticides for controlling e.g. round worm and root worm.
XX	
PS	Claim 60; Page 188-189; 223pp; English.
XX	
CC	The present invention relates to modified potato patatins that maintain
CC	enzymatic and insecticidal activity but which have reduced allergenicity.
CC	Groups (especially Tyr) which bind to anti-patatin antibodies were
CC	identified and glycosylation sites involved in antibody binding were
CC	removed via site directed mutagenesis. The patatins stunt the growth of
CC	larvae so that maturation is prevented or delayed. The patatins also have
CC	non-specific lipid acyl hydrolase activity. The modified patatins are
CC	also useful for inhibiting the activity of corn round worms.
CC	Deallergenised protein can be used as insecticides, as nutritional
CC	supplements and as immunising agents. The present sequence was used to
CC	illustrate the present invention
XX	
SQ	Sequence 366 AA;
	Query Match                      82.8%; Score 1544; DB 4; Length 366;
	Best Local Similarity    100.0%; Pred. No. 2.6e-133; Indels    0; Gaps    0
	Matches    303; Conservative    0; Mismatches    0; Indels       0; Gaps       0
OY	1 SLNFKKMLLSLIGCTTSEFDKTYAKAATTAHMMVLIOKMTDAASSYNTDYLLSTA 60
DB	
	64 SLNFKKMLLSLIGCTTSEFDKTYAKAATTAHMMVLIOKMTDAASSYNTDYLLSTA 123
OY	61 FOALDSKNNYLRVOENALTGTTTMDASBANMELLVVGENVLLKKPVSEDNPETYEAL 120
DB	
	124 FOALDSKNNYLRVOENALTGTTTMDASBANMELLVVGENVLLKKPVSEDNPETYEAL 183
OY	121 KRFAKLSDRKRRLRANKASYGGQUGENVTVLISIDGGGRGIIPATILFLESGQLQEMDN 180
DB	
	184 KRFAKLSDRKRRLRANKASYGGQUGENVTVLISIDGGGRGIIPATILFLESGQLQEMDN 243
OY	181 NADARLADYPVIGTGSTGSLTLTAMISTPENNNRPFAAKEIVPYFEHGPOIFNPSCOI 240
DB	
	244 NADARLADYPVIGTGSTGSLTLTAMISTPENNNRPFAAKEIVPYFEHGPOIFNPSCOI 303
OY	241 LGRPKYDKYLMOVIQEKLGTRRVHQAITEVVISSPDIKTNRKVIFTKSNLANSPELDAM 300
DB	
	304 LGPKYDKYLMQVLOEKGLETGVHQAITEVVISSPDIKTNRKVIFTKSNLANSPELDAM 363
OY	301 YDI 303
DB	364 YDI 366

XX	AC	ADM93064;
XX	AD	ADM93064 standard; protein; 366 AA.
XX	DT	03-JUN-2004 (first entry)
XX	DE	Permutectin protein #3.
XX	KM	lipid acyl hydrolase; corn rootworm; insect infestation; plant;
XX	OS	insect control; nutritional supplement; ds; permutein.
XX	PN	Synthetic.
XX	PD	US6657046-BI.
XX	PP	02-DEC-2003.
XX	PR	05-JAN-2001; 2001US-00755274.
XX	PR	06-JAN-2000; 2000US-0174669P.
XX	PA	21-JUL-2000; 2000US-0219912P.
XX	PI	(MONS ) MONSANTO TECHNOLOGY LLC.
XX	DR	Alibhai MF, Rydel TJ;
XX	DR	WPI; 2004-058368/06.
XX	PT	N-P8DB; ADM93063.
XX	PS	New lipid acyl hydrolase proteins, useful for inhibiting insect
XX	CC	infestation of a plant or plant part, for controlling insects, as
XX	CC	nutritional supplements, or in immunotherapy protocols.
XX	CC	Example 6; SEQ ID NO 25; 73pp; English.
XX	CC	The invention relates to an isolated peptide exhibiting lipid acyl
XX	CC	hydrolase activity and corn rootworm insect inhibitory bioactivity. The
XX	CC	lipid acyl hydrolase peptide is useful for inhibiting insect infestation
XX	CC	of a plant or plant part, for controlling insects (e.g. corn rootworm),
XX	CC	as nutritional supplements, and in immunotherapy protocols. The present
XX	CC	sequence represents the amino acid sequence of permutein.
XX	CC	Sequence 366 AA;
XX	CC	Query Match 82.8%; Score 1544; DB 8; Length 366;
XX	CC	Best Local Similarity 100.0%; Pred. No. 2.6e-133; Mismatches 0; Indels 0; Gaps 0
XX	CC	Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1	SLNKKMLLSLGTTSEPDXTYTAKEATWTAVHMLVIQKMTDAASVTWDYYLSTA 60
DB	64	SLNKKMLLSLGTTSEPDXTYTAKEAATWTAVHMLVIQKMTDAASVTWDYYLSTA 123
QY	61	FQALDSKNVRYVENALTGTTTMDDASEANMELLVOGENILKKPVSEDNPETYEEL 120
DB	124	FQALDSKNVRYVENALTGTTTMDDASEANMELLVOGENILKKPVSEDNPETYEEL 183
QY	121	KRFAKLLSDRKLRLANKASYGPQGLGEWVTYLISIDGGIRGIIPATILLEFLEGQLQEMDN 180
DB	184	KRFAKLLSDRKLRLANKASYGPQGLGEWVTYLISIDGGIRGIIPATILLEFLEGQLQEMDN 243
QY	181	NADARLADYPVIGTSTGGLLTAMIISPENNNRPFAAKEIVPFPEHGPOIFNPSCOI 240
DB	244	NADARLADYPVIGTSTGGLLTAMISTPENNNRPFAAKEIVPFPEHGPOIFNPSCOI 303
QY	241	LGPVKDGYLMOVLQOEKIGTRVQAILEVVISFPDITNKPFVIFTKNTLANSPBLDAXM 300
DB	304	LGPVKDGYLMOVLQOEKIGTRVQAILEVVISFPDITNKPFVIFTKNTLANSPBLDAXM 363
QY	301	YDI 303

DB 364 YDI 366

## RESULT 13

ADM9312 standard; protein; 366 AA.

ADM9312;

28-SEP-2001 (first entry)

Permutate protein #5.

Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity; larva growth; lipid acyl hydrolase; insecticide.

Unidentified.

WO200149834-A2.

12-JUL-2001.

05-JAN-2001; 2001WO-US000342.

06-JAN-2000; 2000US-0174669P.

(MONS ) MONSANTO CO.

Alibhai MF, Atwood JD, Mcwherter CA, Sampson HA;

WPI; 2001-441874/47.

Modified potato patatin proteins with reduced antigenicity, useful as insecticides for controlling e.g. round worm and root worm.

Claim 60; Page 193-194; 223pp; English.

The present invention relates to modified potato patatins that maintain enzymatic and insecticidal activity but which have reduced allergenicity. Groups (especially Tyr) which bind to anti-patatin antibodies were identified and glycosylation sites involved in antibody binding were removed via site directed mutagenesis. The patatins stunt the growth of larvae so that maturation is prevented or delayed. The patatins also have non-specific lipid acyl hydrolase activity. The modified patatins are also useful for inhibiting the activity of corn round worms. Deallerenised protein can be used as insecticides, as nutritional supplements and as immunising agents. The present sequence was used to illustrate the present invention

Sequence 366 AA;

Query Match 79.4%; Score 1480; DB 4; Length 366;

Best Local Similarity 100.0%; Pred. No. 2.1e-127; Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 76 NALTGTTTMDSDSEANMELLVOVGENLLKKPVSEDPETYEALRFAKLSDRKKLRA 135  
DB 1 NALTGTTTMDSDSEANMELLVOVGENLLKKPVSEDPETYEALRFAKLSDRKKLRA 60  
QY 136 NKASVPGQIGENVTVLSDGGIRGIIPATILIEFLGQLOEMDNADARLADYFDVIGG 195  
DB 61 NKASVPGQIGENVTVLSDGGIRGIIPATILIEFLGQLOEMDNADARLADYFDVIGG 120  
QY 196 TSTGGLLTAMISTPNENNRPPAAKEIVPFYFEGHQIFNPSQQLGPKYDGYLMQVLA 255  
DB 121 TSTGGLLTAMISTPNENNRPPAAKEIVPFYFEGHQIFNPSQQLGPKYDGYLMQVLA 180  
QY 256 EKIGETRVHQAALTEVVISFDIKTKPKVIFTKSNLANSELDKAMVDISYSTAAATYFP 315  
DB 181 EKIGETRVHQAALTEVVISFDIKTKPKVIFTKSNLANSELDKAMVDISYSTAAATYFP 240  
QY 316 PHYFVNTNSGDEYEFNLVDGAATVADPALLISVATRLAQKOPAFASIR 366

DB 241 PHYFVNTNSGDEYEFNLVDGAATVADPALLISVATRLAQKOPAFASIR 291

## RESULT 14

ADM93068 standard; protein; 366 AA.

ADM93068;

03-JUN-2004 (first entry)

Permutate protein #5.

lipid acyl hydrolase; corn rootworm; insect infestation; plant; insect control; nutritional supplement; ds; permutate.

Synthetic.

US6657046-B1.

02-DEC-2003.

05-JAN-2001; 2001US-00755274.

06-JAN-2000; 2000US-0174669P.

21-JUL-2000; 2000US-0219912P.

(MONS ) MONSANTO TECHNOLOGY LLC.

Alibhai MF, Rydel TU;

WPI; 2004-058368/06.

N-PADB; ADM93067.

New lipid acyl hydrolase proteins, useful for inhibiting insect infestation of a plant or plant part, for controlling insects, as nutritional supplements, or in immunotherapy protocols.

Example 6; SEQ ID NO 29; 73pp; English.

The invention relates to an isolated peptide exhibiting lipid acyl hydrolase activity and corn rootworm insect inhibitory bioactivity. The lipid acyl hydrolase peptide is useful for inhibiting insect infestation of a plant or plant part, for controlling insects (e.g. corn rootworm), as nutritional supplements, and in immunotherapy protocols. The present sequence represents the amino acid sequence of permutate.

Sequence 366 AA;

Query Match 79.4%; Score 1480; DB 8; Length 366;

Best Local Similarity 100.0%; Pred. No. 2.1e-127; Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 76 NALTGTTTMDSDSEANMELLVOVGENLLKKPVSEDPETYEALRFAKLSDRKKLRA 135  
DB 1 NALTGTTTMDSDSEANMELLVOVGENLLKKPVSEDPETYEALRFAKLSDRKKLRA 60  
QY 136 NKASVPGQIGENVTVLSDGGIRGIIPATILIEFLGQLOEMDNADARLADYFDVIGG 195  
DB 61 NKASVPGQIGENVTVLSDGGIRGIIPATILIEFLGQLOEMDNADARLADYFDVIGG 120  
QY 196 TSTGGLLTAMISTPNENNRPPAAKEIVPFYFEGHQIFNPSQQLGPKYDGYLMQVLA 255  
DB 121 TSTGGLLTAMISTPNENNRPPAAKEIVPFYFEGHQIFNPSQQLGPKYDGYLMQVLA 180  
QY 256 EKIGETRVHQAALTEVVISFDIKTKPKVIFTKSNLANSELDKAMVDISYSTAAATYFP 315  
DB 181 EKIGETRVHQAALTEVVISFDIKTKPKVIFTKSNLANSELDKAMVDISYSTAAATYFP 240  
QY 316 PHYFVNTNSGDEYEFNLVDGAATVADPALLISVATRLAQKOPAFASIR 366  
DB 241 PHYFVNTNSGDEYEFNLVDGAATVADPALLISVATRLAQKOPAFASIR 291

## RESULT 15

AAG99081

ID AAG99081 standard; protein; 367 AA.

XX AAG99081;

AC AAG99081;

XX 28-SEP-2001 (first entry)

DT 28-SEP-2001 (first entry)

XX Pre-cleavage patatin protein #2.

DE Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;

XX larva growth; lipid acyl hydrolase; insecticide.

XX Unidentified.

OS Unidentified.

XX WO200149834-A2.

XX 12-JUL-2001.

PD 12-JUL-2001.

XX 05-JAN-2001; 2001WO-US000342.

PF 05-JAN-2001; 2001WO-US000342.

XX 06-JAN-2000; 2000US-0174669P.

PR 06-JAN-2000; 2000US-0174669P.

XX (MONS ) MONSANTO CO.

XX (MONS ) MONSANTO CO.

PA (MONS ) MONSANTO CO.

XX (MONS ) MONSANTO CO.

XX (MONS ) MONSANTO CO.

PI Alibhai MF, Metwood JD, McWherter CA, Sampson HA;

XX Alibhai MF, Metwood JD, McWherter CA, Sampson HA;

XX WPI; 2001-441874/47.

DR WPI; 2001-441874/47.

XX Modified potato patatin proteins with reduced antigenicity, useful as

PT insecticides for controlling e.g. round worm and root worm.

XX insecticides for controlling e.g. round worm and root worm.

PS Claim 1; Page 138-139; 223pp; English.

XX Claim 1; Page 138-139; 223pp; English.

XX The present invention relates to modified potato patatins that maintain

CC enzymatic and insecticidal activity but which have reduced allergenicity.

CC Groups (especially Tyr) which bind to anti-patatin antibodies were

CC identified and glycosylation sites involved in antibody binding were

CC removed via site directed mutagenesis. The patatins stunt the growth of

CC larvae so that maturation is prevented or delayed. The patatins also have

CC non-specific lipid acyl hydrolase activity. The modified patatins are

CC also useful for inhibiting the activity of corn round worms.

CC Deallergenised protein can be used as insecticides, as nutritional

CC supplements and as immunising agents. The present sequence was used to

CC illustrate the present invention

XX Sequence 367 AA;

SQ Sequence 367 AA;

Query Match 61.1%; Score 1139; DB 4; Length 367;

Best Local Similarity 100.0%; Pred. No. 5.7e-96;

Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 OLGEMVTIVSIDGGIRGIIPATILFLESGQLQEMDNMDARLADYFDVIGTSGILT 203  
 DB 5 QLGEMVTIVSIDGGIRGIIPATILFLESGQLQEMDNMDARLADYFDVIGTSGILT 64  
 QY 204 AMISTPENNNRPFAAKEIVPFYFEHGPQIFNPSGQILGPKYDGKYLMOVLQEKLGSTRV 263  
 DB 65 AMISTPENNNRPFAAKEIVPFYFEHGPQIFNPSGQILGPKYDGKYLMOVLQEKLGSTRV 124  
 QY 264 HQALTEVIVISSFDIKTKNKPVIFTKSNLANSPELDACKYDISYSTAAPTYFPFHYFYNT 323  
 DB 125 HQALTEVIVISSFDIKTKNKPVIFTKSNLANSPELDACKYDISYSTAAPTYFPFHYFYNT 184  
 QY 324 SNGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366  
 DB 185 SNGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 227

Search completed: April 8, 2005, 07:38:50

Job time : 177 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: April 8, 2005, 07:27:49 ; Search time 45 Seconds  
(without alignments)  
782.563 Million cell updates/sec

Title: US-10-658-180-247

Sequence: 1 SLNYKKMLLLSGTGTSEF.....LSISVATRLAQKDPAFASIR 366

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1033	55.4	386	2 A26017	patatin T5 precurs
2	1033	55.4	386	2 S51596	patatin precursor,
3	1017	54.5	386	2 A29810	patatin - potato
4	1014	54.4	386	2 S05592	patatin precursor
5	1014	54.4	386	2 B26017	patatin T58 precu
6	1011	54.2	384	2 A24142	patatin precursor
7	1004	53.8	386	2 T07592	class I patatin -
8	1002	53.7	377	2 S05593	patatin precursor
9	778.5	32.9	390	2 T03841	patatin homolog -
10	614	31.7	414	2 H85437	patatin-like prote
11	612	32.8	410	2 T52294	patatin-like prote
12	575	30.8	414	2 C85437	patatin-like prote
13	569.5	30.5	407	2 T00989	hypothetical prote
14	560	30.0	428	2 F85437	patatin-like prote
15	507.5	27.2	405	2 T10260	patatin-like prote
16	462.5	24.8	388	2 T10765	patatin-like latex
17	454.5	24.4	388	2 T10763	patatin-like latex
18	450.5	24.2	388	2 T10770	patatin-like latex
19	288.5	15.5	390	2 AG2093	patatin-like prote
20	284.5	15.3	499	2 T02580	hypothetical prote
21	275.5	14.8	488	2 T06725	hypothetical prote
22	257.5	13.8	526	2 T08541	hypothetical prote
23	243	13.0	382	2 T84109	hypothetical prote
24	212	11.6	355	2 B82354	patatin-related pr
25	198	10.6	490	2 B87815	patatin b1 precurs
26	189	10.1	1023	2 T26261	hypothetical prote
27	185.5	9.9	679	2 G71615	phospholipase A2-1
28	177	9.5	494	2 D71655	patatin b1 precurs
29	159	8.5	60	2 A23634	patatin precursor

30	148	7.9	56	2 S08631	patatin PG13 - pot
31	146.5	7.9	468	2 T33857	hypothetical prote
32	143.5	7.7	456	2 T24442	hypothetical prote
33	135	7.2	1265	2 T02131	hypothetical prote
34	134	7.2	851	2 T12503	hypothetical prote
35	128	6.9	782	2 UC7284	phospholipase A2 (
36	125.5	6.7	1071	2 T22327	hypothetical prote
37	117.5	6.3	431	2 D87608	hypothetical prote
38	113.5	6.1	447	2 AD0168	probable Arpase pr
39	113.5	6.1	826	2 T06036	hypothetical prote
40	109.5	5.9	1237	2 D71850	probable outer mem
41	109	5.8	320	2 F70034	conserved hypochet
42	109	5.8	1048	2 A70592	hypothetical prote
43	108	5.8	845	1 GLVK	beta-glucosidase (
44	107.5	5.8	318	2 S24923	REG protein - Bac
45	107.5	5.8	901	2 S50987	SOK1 protein - Yea

## ALIGNMENTS

### RESULT 1

A26017 patatin T5 precursor - potato

C/Species: Solanum tuberosum (potato)

C/Date: 05-Oct-1988 #sequence\_revision 05-Oct-1988 #text\_change 09-Jul-2004

C/Accession: A26017

R/Rosahl, S.; Schmidt, R.; Scheil, J.; Willmitzer, L.

Mol. Gen. Genet. 203, 214-220, 1986

A/Title: Isolation and characterization of a gene from Solanum tuberosum encoding patatin

A/Reference number: A26017

A/Accession: A26017

A/Molecule type: DNA

A/Residues: 1-386 <ROS>

A/Cross-references: UNIPROT:P15478

C/Superfamily: patatin

Query Match 55.4%; Score 1033; DB 2; Length 386;

Best Local Similarity 90.1%; Pred. No. 2.9e-67;

Matches 200; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

Qy	145	IGENWTVLSIDGGIRGIRIPATILFLEGLQLOEMDNADRLADYDPVIGSTGSLITA	204
Db	25	IGENWTVLSIDGGIRKIIIPATILFLEGLQLOEDNNTDARLADYDPVIGSTGSLITA	84
Qy	205	MISTPENNNRPPAAAKIIVPFYFHEHGPQIFNPSGQILGPKYDKYLMQVLOEKLGRTVH	264
Db	85	MITPENETNRPFAAKDIVEFYFHEHGPKIFOSSGSIFGPYDKYLMQVLOEKLGRTVH	144
Qy	265	QALTEVVISFDTKTNKEVIFETSNLANSPELDAXWDISYTAAPTFPPHYFVNTS	324
Db	145	QALTEVAISSFDIKTNKPVIFETSNLAKSPDLAKMDICYSTAAATFPPHYFVNTS	204
Qy	325	NGDEYEFNLVDGAVATVADPALISISVATRLAQKDPAFASIR	366
Db	205	NGDKYEFNLVDGAVATVDDPALISISVATRLAQVDPKFAIRK	246

### RESULT 2

S51596 patatin precursor, non-sucrose-inducible - Solanum brevifidens

C/Species: Solanum brevifidens

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C/Accession: S51596

R/Banfalvi, Z.; Kozllyal, Z.; Barta, E.

Mol. Gen. Genet. 245, 517-522, 1994

A/Title: Solanum brevifidens possesses a non-sucrose-inducible patatin gene.

A/Reference number: S51596; MUID:95107249; EMD:7808402

A/Accession: S51596

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-386 <BAN>

A/Cross-references: UNIPROT:Q42502; EMBL:U09331; NID:9563124; P1DN:AAA66198.1; P1D:956312;

C/Superfamily: patatin  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-386/Product: patatin #status predicted <MAT>

Query Match 55.4%; Score 1033; DB 2; Length 386;  
Best Local Similarity 89.6%; Pred. No. 2,9e-67;  
Matches 199; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 145 LGEMVTVLISIDGGIRGIIPATILEFLLEGQLQEMDNADARLADYFDVIGSTGGLLT 204  
DB 25 LGEMVTVLISIDGGIRGIIPATILEFLLEGQLQEVNNDKARLADYFDVIGSTGGLLT 84  
QY 205 MISTPENNRPFAAKEIVPFYFEHGPQIFNPSGQILGPKYDGKYLQVLOEKLGETRV 264  
DB 85 MISTPENNRPFAAKDIVPFYFEHGPPIFNYSGSILGPMYDGKYLQVLOEKLGETRV 144  
QY 265 QALTEVAISSFDIKTNKPVIFTKSNLANSPELDAMVDISYSTAAAPTYFPFHYVTNT 324  
DB 145 QALTEVAISSFDIKTNKPVIFTKSNLAKSPELDAMVDICYSTAAAPTYFPFHYVTNT 204  
QY 325 NGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366  
DB 205 NGDEYEFNLVDGAVATVADPALISVATRLAQVDPKPFASIR 246

## RESULT 3

A29810  
patatin - potato  
C/Species: Solanum tuberosum (potato)  
C/Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C/Accession: A29810  
R/Mignery, G.A.; Pikaard, C.S.; Park, W.D.  
Gene 62, 27-44, 1988

A/Title: Molecular characterization of the patatin multigene family of potato.

A/Reference number: A29810; MUID:88226014; PMID:3371664

A/Accession: A29810

A/Molecule type: DNA

A/Residues: 1-386 <MTG>

A/Cross-references: UNIPROT:P11768; GB:M18880; NID:G169499; PIDN:AAA3819.1; PID:G169500

C/Genetics:

A/Intons: 56/3; 117/2; 169/3; 224/3; 320/3; 368/2

C/Superfamily: patatin

Query Match 54.5%; Score 1017; DB 2; Length 386;  
Best Local Similarity 87.9%; Pred. No. 4.2e-66;  
Matches 196; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 144 QLGEMVTVLISIDGGIRGIIPATILEFLLEGQLQEMDNADARLADYFDVIGSTGGLLT 203  
DB 24 KLEEMVTVLISIDGGIRGIIPATILEFLLEGQLQEVNNDKARLADYFDVIGSTGGLLT 83  
QY 204 AMISTPENNRPFAAKEIVPFYFEHGPQIFNPSGQILGPKYDGKYLQVLOEKLGETRV 263  
DB 84 AMISTPENNRPFAAKDIVPFYFEHGPPIFNYSGSILGPMYDGKYLQVLOEKLGETRV 143  
QY 264 HQALTEVAISSFDIKTNKPVIFTKSNLANSPELDAMVDISYSTAAAPTYFPFHYVTNT 323  
DB 144 HQALTEVAISSFDIKTNKPVIFTKSNLAKSPELDAMVDICYSTAAAPTYFPFHYVTNT 203  
QY 324 SNGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366  
DB 204 SNGDEYEFNLVDGAVATVADPALISVATRLAQEDPAPASIR 246

## RESULT 4

S05592  
patatin precursor (clone pPATB2) - potato  
C/Species: Solanum tuberosum (potato)  
C/Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004  
C/Accession: S05592

R/Stiekema, W.J.; Heidkamp, F.; Dirkse, W.G.; van Beckum, J.; de Haan, P.; ten Bosch, C.  
Plant Mol. Biol. 11, 255-269, 1988  
A/Title: Molecular cloning and analysis of four potato tuber mRNAs.

A/Reference number: S05592  
A/Accession: S05592  
A/Molecule type: mRNA  
A/Residues: 1-386 <STI>  
A/Cross-references: UNIPROT:P15477; EMBL:X13178; NID:G21509; PIDN:CAA1575.1; PID:G21510  
A/Note: the authors translated the codon CAG for residue 288 as Glu and CAA for residue 2  
C/Superfamily: patatin  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-386/Product: patatin #status predicted <MAT>

Query Match 54.4%; Score 1014; DB 2; Length 386;  
Best Local Similarity 88.3%; Pred. No. 7e-66;  
Matches 197; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 144 QLGEMVTVLISIDGGIRGIIPATILEFLLEGQLQEMDNADARLADYFDVIGSTGGLLT 203  
DB 24 KLEEMVTVLISIDGGIRGIIPATILEFLLEGQLQEVNNDKARLADYFDVIGSTGGLLT 83  
QY 204 AMISTPENNRPFAAKEIVPFYFEHGPQIFNPSGQILGPKYDGKYLQVLOEKLGETRV 263  
DB 84 AMISTPENNRPFAAKDIVPFYFEHGPPIFNYSGSILGPMYDGKYLQVLOEKLGETRV 143  
QY 264 HQALTEVAISSFDIKTNKPVIFTKSNLANSPELDAMVDISYSTAAAPTYFPFHYVTNT 323  
DB 144 HQALTEVAISSFDIKTNKPVIFTKSNLAKSPELDAMVDICYSTAAAPTYFPFHYVTNT 203  
QY 324 SNGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366  
DB 204 SNGARIEFNLVDGAVATVADPALISVATRLAQEDPAPASIR 246

## RESULT 5

B26017  
patatin T58 precursor - potato  
C/Species: Solanum tuberosum (potato)  
C/Date: 03-Nov-1987 #sequence\_revision 03-Nov-1987 #text\_change 09-Jul-2004  
C/Accession: B26017  
C/Rosahl, S.; Schmidt, R.; Schell, J.; Willmitzer, L.  
Mol. Gen. Genet. 203, 214-220, 1986

A/Title: Isolation and characterization of a gene from Solanum tuberosum encoding patatin

A/Reference number: A26017

A/Accession: B26017

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-386 <ROS>

A/Cross-references: UNIPROT:Q41467

C/Superfamily: patatin

Query Match 54.4%; Score 1014; DB 2; Length 386;  
Best Local Similarity 88.3%; Pred. No. 7e-66;  
Matches 197; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 144 QLGEMVTVLISIDGGIRGIIPATILEFLLEGQLQEMDNADARLADYFDVIGSTGGLLT 203  
DB 24 KLEEMVTVLISIDGGIRGIIPATILEFLLEGQLQEVNNDKARLADYFDVIGSTGGLLT 83  
QY 204 AMISTPENNRPFAAKEIVPFYFEHGPQIFNPSGQILGPKYDGKYLQVLOEKLGETRV 263  
DB 84 AMISTPENNRPFAAKDIVPFYFEHGPPIFNYSGSILGPMYDGKYLQVLOEKLGETRV 143  
QY 264 HQALTEVAISSFDIKTNKPVIFTKSNLANSPELDAMVDISYSTAAAPTYFPFHYVTNT 323  
DB 144 HQALTEVAISSFDIKTNKPVIFTKSNLAKSPELDAMVDICYSTAAAPTYFPFHYVTNT 203  
QY 324 SNGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366  
DB 204 SNGARIEFNLVDGAVATVADPALISVATRLAQEDPAPASIR 246

## RESULT 6

A24142  
patatin precursor - potato  
C/Species: Solanum tuberosum (potato)

C>Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 09-Jul-2004  
C/Accession: A24142; S54829  
R/Bevan, M.; Barker, R.; Goldbrough, A.; Jarvis, M.; Kavanagh, T.; Iturriaga, G.  
Nucleic Acids Res. 14, 4625-4638, 1986  
A/Title: The structure and transcription start site of a major potato tuber protein gene  
A/Reference number: A24142; PMID:86232596; PMID:3714488  
A/Accession: A24142  
A/Molecule type: DNA  
A/Residues: 1-384 <BEV>  
A/Cross-references: UNIPROT:Q9SAP2  
R/Zhu, Y.; Dai, W.L.; Liu, J.; Zhao, S.Y.; Wang, X.M.  
submitted to the EMBL Data Library, May 1995  
A/Description: Isolation and sequence of class I patatin gene from a Chinese potato cult  
A/Reference number: S54829  
A/Accession: S54829  
A/Molecule type: DNA  
A/Residues: 1-56, 'p' <ZHU>  
A/Cross-references: EMBL:X67216; NID:G809604; PIDN:CAA60675.1; PID:G809605  
A/Experimental source: clone 22-1; cultivar Dongnong 303  
C/Genetics:  
A/Intons: 56/3; 117/3; 169/3; 224/3; 320/3; 368/3  
C/Superfamily: patatin  
F/1-23/Domain: signal sequence #status predicted <SIG>  
F/24-384/Product: patatin #status predicted <MAT>

Query Match 54.2%; Score 1011; DB 2; Length 384;  
Best Local Similarity 87.8%; Pred. No. 1.1e-65;  
Matches 195; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 145 LGEMVTVLSIDGGIGIIPATILEFLEGQLOEMDNADARLADYFDVIGSTGGLTTA 204  
DB 25 LGEMVTVLSIDGGIGIIPATILEFLEGQLOEVNNDKARLADYFDVIGSTGGLTTA 84  
QY 205 MISTPENNRPPAAKEIVPFYFEHGPQIFNPSGQILGPKYDKYLMQVLQEKLGSTRVH 264  
DB 85 MITTPENNRPPAAKDIYVFFYEHGPHIFNYRSGISGPRYDGKYLQVLQEKLGSTRVH 144  
QY 265 QALTEVVISFDIKTKKPVIFTKSNLANSPELDARKYDYSYTAAPTYPPHYFVNTS 324  
DB 145 QALTEVAISSFDIKTKKPVIFTKSNLANSPOLDARKYDICTAADIYPPPHFVHTS 204  
QY 325 NGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366  
DB 205 NGATYEFNLVDGAVATVADPALISVATRLAQEDPAPASSIK 246

RESULT 7  
T07592  
class I patatin - potato  
C/Species: Solanum tuberosum (potato)  
C/Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C/Accession: T07592  
R/Yang, M.S.  
submitted to the EMBL Data Library, November 1993  
A/Reference number: Z16035  
A/Accession: T07592  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: mRNA  
A/Residues: 1-386 <YAN>  
A/Cross-references: UNIPROT:Q41487; EMBL:Z27221; NID:G695755; PIDN:CAA81735.1; PID:G6957  
A/Experimental source: cv. Sunn; mature plants  
A/Note: cDNA, isolated from potato cultivated in Korea  
C/Superfamily: patatin

Query Match 53.8%; Score 1004; DB 2; Length 386;  
Best Local Similarity 89.2%; Pred. No. 3.7e-65;  
Matches 198; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 145 LGEMVTVLSIDGGIGIIPATILEFLEGQLOEMDNADARLADYFDVIGSTGGLTTA 204  
DB 25 LGEMVTVLSIDGGIGIIPATILEFLEGQLOEMDNADARLADYFDVIGSTGGLTTA 84  
QY 205 MISTPENNRPPAAKEIVPFYFEHGPQIFNPSGQILGPKYDKYLMQVLQEKLGSTRVH 264

DB 85 MITTPENNRPPAAKEIVPFYFEHGPQIFNPSGQIFRKYDKYLMQVLQEKLGSTRVH 144  
QY 265 QALTEVVISFDIKTKKPVIFTKSNLANSPELDARKYDYSYTAAPTYPPHYFVNTS 324  
DB 145 QALTEVAISSFDIKTKKPVIFTKSNLANSPELDARKYDICTAADIYPPPHFVHTS 204  
QY 325 NGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366  
DB 205 NGATYEFNLVDGAVATVADPALISVATRLAQEDPAPASSIK 246

RESULT 8  
S05593  
patatin precursor (clone pPAT1) - potato (fragment)  
N/Contains: proteinase inhibitor II  
C/Species: Solanum tuberosum (potato)  
C/Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004  
C/Accession: S05593  
R/Stiekema, W.J.; Heidkamp, F.; Dirkse, W.G.; van Beckum, J.; de Haan, P.; ten Bosch, C.  
Plant Mol. Biol. 11, 255-269, 1988  
A/Title: Molecular cloning and analysis of four potato tuber mRNAs.  
A/Reference number: S05592  
A/Accession: S05593  
A/Molecule type: mRNA  
A/Residues: 1-377 <STI>  
A/Cross-references: UNIPROT:P15476; EMBL:X13179; NID:G21507; PIDN:CAA31576.1; PID:G80506;  
A/Note: the authors translated the codon CAG for residue 288 as Glu and CAA for residue 2  
C/Superfamily: patatin  
F/1-14/Domain: signal sequence (fragment) #status predicted <SIG>  
F/15-377/Product: patatin #status predicted <MAT>

Query Match 53.7%; Score 1002; DB 2; Length 377;  
Best Local Similarity 87.0%; Pred. No. 5e-65;  
Matches 194; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 144 QLGEMVTVLSIDGGIGIIPATILEFLEGQLOEMDNADARLADYFDVIGSTGGLTT 203  
DB 15 KLEEMVTVLSIDGGIGIIPATILEFLEGQLOEVNNDKARLADYFDVIGSTGGLTT 74  
QY 204 AMISTPENNRPPAAKEIVPFYFEHGPQIFNPSGQILGPKYDKYLMQVLQEKLGSTRV 263  
DB 75 AMITTPENNRPPAAANDIYVFFYEHGPHIFNYRSGISGPRYDGKYLQVLQEKLGSTRV 134  
QY 264 HQALTEVVISFDIKTKKPVIFTKSNLANSPELDARKYDYSYTAAPTYPPHYFVNTS 323  
DB 135 HQALTEVAISSFDIKTKKPVIFTKSNLANSPELDARKYDICTAADIYPPPHFVHTS 194  
QY 324 NGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366  
DB 195 NGATYEFNLVDGAVATVADPALISVATRLAQEDPAPASSIK 237

RESULT 9  
T03841  
patatin homolog - common tobacco  
C/Species: Nicotiana tabacum (common tobacco)  
C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C/Accession: T03841  
R/Drews, G.N.; Beale, T.P.; Bul, A.Q.; Goldberg, R.B.  
Plant Cell 4, 1383-1404, 1992  
A/Title: Regional and cell-specific gene expression patterns during petal development.  
A/Reference number: Z15112; PMID:93120883; PMID:1477354  
A/Accession: T03841  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: mRNA  
A/Residues: 1-390 <DBE>  
A/Cross-references: UNIPROT:O24152; EMBL:U68484; NID:G1546816; PIDN:AA08428.1; PID:G1546  
C/Superfamily: patatin

Query Match 41.7%; Score 778.5; DB 2; Length 390;  
Best Local Similarity 67.1%; Pred. No. 8.1e-49;  
Matches 151; Conservative 31; Mismatches 36; Indels 7; Gaps 4;





T00989  
hypothetical protein Atg26560 [imported] - Arabidopsis thaliana  
N/Alternate names: patatin homolog T9J22.23  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C/Accession: T00989; A84662  
R/Rounstey, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kauli  
submitted to the EMBL Data Library, April 1998  
A/Description: Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence.  
A/Reference number: Z14161  
A/Accession: T00989  
A/Status: translated from GB/EMBL/DDBJ  
A/Molecule type: DNA  
A/Residues: 1-407 <ROU>  
A/Cross-references: UNIPROT:O48723; EMBL:AC002505; NID:g2739359; PIDN:AAC14504.1; PID:g2739359; NCBI:U00001.1; PDB:1ZGQ  
A/Experimental source: cultivar Columbia  
R/Lin, X.; Kaul, S.; Rounstey, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M., Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vancken, S.E.; Unayem, L.; Tallon, L.;  
euse, D.; Niernann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: A84662  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-407 <STO>  
A/Cross-references: GB:AE002093; NID:g2739381; PIDN:AC14504.1; GSPDB:GN00139  
C/Genetics:  
A/Gene: Atg26560; T9J22.23  
A/Map position: 2  
A/Intons: 46/3; 169/3; 223/3; 324/3; 382/2  
C/Superfamily: patatin

Query Match 30.5%; Score 569.5; DB 2; Length 407;  
Best Local Similarity 51.8%; Pred. No. 1.2e-33;  
Matches 118; Conservative 32; Mismatches 65; Indels 13; Gaps 3;

DY 137 KASYGPQLGEMVTVLSIDGGIRGLIPATILFLEGLQEMDNADARLADYFDVIGT 196  
Db 7 KSLPQPPTGVNLVTILSIDGGIRGLIPAVILGFLESFLQLKLDGS-EARLADYFDVIAGT 65

DY 197 STGGLINAMISTPNENRRPPAAAKEIVPFYEHGPOITNS-----GQILPKY 245  
Db 66 STGGIIVTAMLTAAPNKCEGRPLFAASEIKDFYLEOCPEKIFPDHPFPSAKKLVKSLTGPKY 125

DY 246 DGKTIQVLQELGETRVHQALETEVISSPDIKNKPVPFTKSNLANSELDAMVDISY 305  
Db 126 DGKTIHQILHAKKLGDTKLSQTLLTNVVLPFTFIKHQLPTFSSEYKQHPLKDQATLADIAT 185

DY 306 STAATPFPFFPHYEVNTSNGDEVEFNLDVAVAVTVADPALSLISVAT 353  
Db 186 STSAAPTLLPAHFPRFKVEDLNCAKEYNMLIDGVA-ANNPALLAIGEVT 232

RESULT 14  
F85437  
patatin-like protein [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: F85437  
R/anonymus, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
Nature 402, 769-777, 1999  
A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A/Reference number: AB5001; MUID:20083488; PMID:10617198  
A/Accession: F85437  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-428 <STO>  
A/Cross-references: UNIPROT:O23181; GB:NC\_001268; NID:g2720654; PIDN:CAB80371.1; GSPDB:G  
C/Genetics:  
A/Gene: ATAg37050  
A/Map position: 4  
C/Superfamily: patatin

[illegible]

```

RESULT 15
T10260
patatin-like protein - cucumer (fragment)
C:Species: Cucumis sativus (cucumber)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10260
R:Preisig-Mueller, R.; May, C.; Hoehne, M.; Gnan, P.; Kindl, H.
submitted to the EMBL Data Library, April 1997
A:Description: Is the patatin-like protein localized to lipid bodies involved in the mobil
A:Reference number: Z17002
A:Accession: T10260
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-405 <PRE-
A:Cross-references: UNIPROT:O23784; EMBL:Y12793
C:Function:
A:Experimental source: cocolledon
C:Superfamily: patatin
A:Description: mobilization of fat during seed germination

Query Match      27.2%; Score 507.5; DB 2; Length 405;
Best Local Similarity 46.8%; Pred. No. 3..7e-29;
Matches 103; Conservative 44; Mismatches 60; Indels 13; Gaps 3;

QY      146 GEMWVVLSDGGGIGIIPATILFLPSQLOEMDNADRLAPYVIGSTGGLTLM 205
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      21 GEMITLSDGGIGIIPSTILAPLESKLEQID- GPDVRIADYFDVIAGTSTGGLVTSM 79

DB      206 ISTPENNRPPFAAKRIVPFVEHGPQIF-----NPSGQLGPKYDGKYLMOVL 254
      ::|||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
DB      80 LTPADKNRPLYSADDLAFYIEHAPKIFPQNRNYFLCSLVNFGKXMGPKYNGIYLRSLI 139
      :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY      255 QKLGSTRVQALTEVIVISSFDIKTNKPVIFTKSNLANSPELDARWYDISYTPAAPTFF 314
      :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
DB      140 KGLLDGITLKQLTSLQVPIPAFDIKLQPIVFTTIEAKCELSKMPKLVADVCISTSAAPTFL 199
      :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY      315 PRHYFVNTNSNGDYEFENLVDAVATVADPALISIVAR 354
      :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
DB      200 PGEYFQTKDSKGINRYEYWDGVA-ANNPTLAAHVTIK 238
      :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:

```

Search completed: April 8, 2005, 07:57:03  
Job time : 46 secs

A;Gene: AT4g37050  
A;Map position: 4  
C;Superfamily: patatin

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: April 8, 2005, 07:26:08 ; Search time 182 Seconds  
(without alignments)  
1029.786 Million cell updates/sec

Title: US-10-658-180-247

Perfect score: 1865

Sequence: 1 SLNKKMALLSLGCTTSEF.....LSISVATRLAQDPAFASIR 366

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1139	61.1	386	2	Q8LPW4 solanum car
2	1033	55.4	386	1	PAT5 SOLTU
3	1033	55.4	386	2	Q42502 solanum tub
4	1033	55.4	386	2	Q42502 solanum tub
5	1017	54.5	386	1	Q7DMP8 solanum bre
6	1014	54.4	386	1	PAT0 SOLTU
7	1014	54.4	386	1	PAT2 SOLTU
8	1004	53.8	386	2	Q41487 solanum tub
9	1002	53.7	377	1	PAT1 SOLTU
10	1002	53.7	386	2	Q41467 solanum tub
11	996.5	53.4	387	2	Q8LSC1 solanum cha
12	778.5	41.7	263	2	Q7DMC7 solanum cha
13	778.5	41.7	390	2	Q24152 nicotiana t
14	614	32.9	383	2	Q8LBT5 arabidopsis
15	614	32.9	414	2	Q23179 arabidopsis
16	613	32.9	420	2	Q9FZ09 nicotiana t
17	612	32.8	410	2	Q23148 arabidopsis
18	609.5	32.7	405	2	Q6ZUD3 oryza sativ
19	585	31.4	387	2	Q67121 oryza sativ
20	579	31.0	400	2	Q9AQT8 oryza sativ
21	575	30.8	414	2	Q23180 arabidopsis
22	569.5	30.5	405	2	Q8LDB8 arabidopsis
23	569.5	30.5	407	2	Q48723 arabidopsis
24	560	30.0	428	2	Q23181 arabidopsis
25	545	29.2	442	2	Q8GVV8 oryza sativ
26	544.5	29.2	431	2	Q6ZG42 oryza sativ
27	543	29.1	411	2	Q9FZ08 nicotiana t
28	537.5	28.8	430	2	Q6ZG46 oryza sativ
29	529.5	28.4	207	2	Q9FZ07 nicotiana t
30	527	28.3	401	2	Q9FIY1 arabidopsis
31	525.5	28.2	410	2	Q9XE75 sorghum bic

32	515	27.6	422	2	Q9XE77 sorghum bic
33	511	27.4	411	2	Q8S0B1 oryza sativ
34	507.5	27.2	405	2	Q23784 cucumis sat
35	494.5	26.5	432	2	Q840Y3 oryza sativ
36	491.5	26.4	438	2	Q9XE79 sorghum bic
37	462.5	24.8	388	2	Q81984 hevea bras
38	458.5	24.6	387	2	Q706V4 hevea bras
39	458.5	24.6	388	2	Q9SEM0 hevea bras
40	454.5	24.4	388	2	Q65811 hevea bras
41	450.5	24.2	388	2	Q04008 hevea bras
42	341.5	18.3	339	2	Q813P2 arabidopsis
43	288.5	15.5	302	2	Q8YUN7 arabidopsis
44	287	15.4	302	2	Q73HJ4 wolbachia sp
45	284.5	15.3	499	2	Q80959 arabidopsis

## ALIGNMENTS

## RESULT 1

ID	Q8LPW4	PRELIMINARY;	PRT;	386 AA.
AC	Q8LPW4			
DT	01-OCT-2002 (TREMREL. 22, Created)			
DT	01-OCT-2002 (TREMREL. 22, Last sequence update)			
DT	01-MAR-2004 (TREMREL. 26, Last annotation update)			
DE	Patacin.			
OS	Solanum cardiophyllum.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OX	lamids; Solanales; Solanaceae; Solanum.			
NCBI_TaxID=160510;				
SEQUENCE FROM N.A.				
MEBLINE=22664533; PubMed=1279324; DOI=10.1021/bi027156r;				
Rydell T.J., Williams J.M., Krieger E., Moshiri F., Stallings W.C.,				
Brown S.M., Pershing J.C., Purcell J.P., Alibhai M.F.;				
"The crystal structure, mutagenesis, and activity studies reveal that				
patacin is a lipid acyl hydrolase with a Ser-Asp catalytic dyad."				
Biochemistry 42:6696-6708(2003).				
[2]				
SEQUENCE FROM N.A.				
Joyce E.K., Levine B., Isaac B., Brown S.M., Pershing J.C.,				
Purcell J.P., Alibhai M.F.;				
Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.				
EMBL; AY033231; AAK5395.1; -				
PDB; 1OXW; X-ray; A/B/C=14-386.				
GO; GO:0003824; F:catalytic activity; IEA.				
GO; GO:0045735; F:nutrient reservoir activity; IEA.				
Interpro: IPR002641; Patacin.				
Pfam: PF01734; Patacin.1				
SEQUENCE 386 AA; 42486 MW; 30C56BA86A024282 CRC64;				

Query Match 61.1%; Score 1139; DB 2; Length 386;  
Best Local Similarity 100.0%; Pred. No. 4.9e-69;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	144	QLGEMTVLISIDGGIRGIIPATILFEFLGQLQEMDNADRLADYDVIGSTGILLT	203
DB	24	QLGEMTVLISIDGGIRGIIPATILFEFLGQLQEMDNADRLADYDVIGSTGILLT	83
QY	204	AMSTPENNRPFAAAKEIYFPFEGHPOIFNSGQILGKYGKYMOVLQELGSTRV	263
DB	84	AMSTPENNRPFAAAKEIYFPFEGHPOIFNSGQILGKYGKYMOVLQELGSTRV	143
QY	264	HOALTEVVISFDIKTKPVIFTKSNLANSPELDAXKYDISYTAAPYFPFHYVTNT	323
DB	144	HOALTEVVISFDIKTKPVIFTKSNLANSPELDAXKYDISYTAAPYFPFHYVTNT	203
QY	324	SNDEYEFNVDGAVATVADPALLISVATRLAQDPAFASIR	366
DB	204	SNDEYEFNVDGAVATVADPALLISVATRLAQDPAFASIR	246

```

RESULT 2
PATS_SOLTU STANDARD; PRT; 386 AA.
ID PAT5_SOLTU STANDARD; PRT; 386 AA.
AC P15478;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Patatin T5 precursor (Potato tuber protein).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RA Rosahl S., Schmidt R., Schell J., Willmitzer L.;
RT "Isolation and characterization of a gene from Solanum tuberosum
RT encoding patatin, the major storage protein of potato tubers."
RL Mol. Gen. Genet. 203:214-220(1986).
CC -1- FUNCTION: Patatin may have a dual role as a somatic storage
CC protein and as an enzyme involved in host resistance. This tuber
CC protein represents approximately 40% of the total protein in
CC mature tubers.
CC -1- MISCELLANEOUS: There is strong evidence that patatin is a
CC lipolytic acyl hydrolase (LAH), an activity which is thought to be
CC involved in the response of tubers to pathogens.
CC -----
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CC -----
DR EMBL, X03932; CA27571.1; -.
DR PIR, A26017; A26017.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.
KM Glycoprotein; Hydrolyase; Multigene family; Signal; Storage protein.
FT CHAIN 1 23
FT SIGNAL 1 23
FT CARBOHYD 24 386
FT CARBOHYD 60 60 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 202 202 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 386 AA; 42338 MW; E7F7PADLA04A1000 CRC64;

Query Match 55.4%; Score 1033; DB 1; Length 386;
Best Local Similarity 90.1%; Pred. No. 7.5e-62;
Matches 200; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

145 LGEWTVLISIDGGIRGIIIPATILEFLEGQLOEMDNADRLADYDPVIGSTGSLTLTA 204
|||||
25 LGEWTVLISIDGGIRGIIIPATILEFLEGQLOEMDNADRLADYDPVIGSTGSLTLTA 84
|||||
205 MISTPENNRPPFAAKEIVPFYFEGHPQIFNPSGQILGPKYDKYLMQVLQEKLGSTRVH 264
|||||
85 MITTPENNRPPFAAKDIPVFPYFEGHPKIFQSSGSIIGPKYDKYLMQVLQEKLGSTRVH 144
|||||
265 QALTEVVISFDIKTKKPYIFTKSNLANSPELDKMYDISYTRAAFTYPPHYFVNTS 324
|||||
145 QALTEVAISSFDIKTKKPYIFTKSNLAKSPELDAMKIDICYSYTAAPTFFPHYFATNTS 204
|||||
325 NGDEYFENLVGAVATVADPALISVATRLAQKDPAFASIR 366
|||||
205 NGDKYFENLVGAVATVADPALISVATRLAQVDPKFAPIK 246
|||||

RESULT 3
042502 PRELIMINARY; PRT; 386 AA.
AC 042502;

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DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Patatin precursor.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85062793; PubMed=6150463;
RA Mignery G.A., Piskard C.S., Hannapel D.J., Park W.D.;
RT "Isolation and sequence analysis of cDNAs for the major potato tuber
RT protein, patatin."
RL Nucleic Acids Res. 12:7987-8000(1984).
DR EMBL; X01125; CA25592.1; -.
DR PIR; S51596; S51596.
DR HSP; Q8LPM4; 10XW.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.
KM Signal.
FT CHAIN 1 23
FT SIGNAL 1 23
FT CHAIN 24 386
SQ SEQUENCE 386 AA; 42465 MW; 178107C161B7DEBD CRC64;

Query Match 55.4%; Score 1033; DB 2; Length 386;
Best Local Similarity 89.6%; Pred. No. 7.5e-62;
Matches 199; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

145 LGEWTVLISIDGGIRGIIIPATILEFLEGQLOEMDNADRLADYDPVIGSTGSLTLTA 204
|||||
25 LGEWTVLISIDGGIRGIIIPATILEFLEGQLOEMDNADRLADYDPVIGSTGSLTLTA 84
|||||
205 MISTPENNRPPFAAKEIVPFYFEGHPQIFNPSGQILGPKYDKYLMQVLQEKLGSTRVH 264
|||||
85 MITTPENNRPPFAAKDIPVFPYFEGHPKIFQSSGSIIGPKYDKYLMQVLQEKLGSTRVH 144
|||||
265 QALTEVVISFDIKTKKPYIFTKSNLANSPELDKMYDISYTRAAFTYPPHYFVNTS 324
|||||
145 QALTEVAISSFDIKTKKPYIFTKSNLAKSPELDAMKIDICYSYTAAPTFFPHYFATNTS 204
|||||
325 NGDEYFENLVGAVATVADPALISVATRLAQKDPAFASIR 366
|||||
205 NGDKYFENLVGAVATVADPALISVATRLAQVDPKFAPIK 246
|||||

RESULT 4
07DMP8 PRELIMINARY; PRT; 386 AA.
ID 07DMP8;
AC 07DMP8;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Patatin precursor.
OS Solanum brevifolius.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4115;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95107249; PubMed=7808402;
RA Banfalvi Z., Kostyal Z., Barta E.;
RT "Solanum brevifolius possesses a non-sucrose-inducible patatin gene."
RL Mol. Gen. Genet. 245:517-522(1994).
DR EMBL; U09331; AA66198.1; -.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.

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KM	Signal.	1	23	Potential.
FT	CHAIN	24	386	patacin.
SQ	SEQUENCE	386 AA;	42465 MW;	178107C161B7DEBD CRC64;
	Query Match		55.4%;	Score 1033; DB 2; Length 386;
	Best Local Similarity		89.6%;	Pred. No. 7.5e-62;
	Matches 199;	Conservative	10;	Mismatches 13; Indels 0; Gaps 0;
QY		145	LGEWTVLISIDGGIRGIIIPATILEFLEGOLOEMDNNDARLADYEDVIGSTSGLLTA	204
Dd		25	LGEWTVLISIDGGIKGIIPATILEFLEGOLOEVNNDARLADYEDVIGSTSGLLTA	84
QY		205	MISTPENNRRPPAAAKEIVPEYFEFGPOLFNPSGCIILPKPIDGKTLMOYLQEKLGTRYH	264
Dd		85	MITTPENNRNPFAAKDVPPEYFEFGPHI FNSGSGIFGPMDYGKFLVLQEKLGTRYH	144
QY		265	QALREVIYSSPDITKNKPVIPTFKSLASPDLDAWYOISYSTAAPYPHPHYEVTMS	324
Dd		145	QALREVALISSPDITKNKPVITFKSLASPELDAMMYICSYTAPAPYFPHPHYVHTS	204
QY		325	NGDEVEFNLVDGA VATVADPALLSISVSTRLAOKDPAPASIR	366
Dd		205	NGDYEFNLVDGA VATVGD PALLSISVATKLAQVDPKRASIK	246
	RESULT 5			
	PAT3 SOLUTU	ID	PAT3 SOLUTU	STANDARD; PR3; 386 AA.
AC		P11768;		
DT		01-APR-1990 (Rel. 14, Created)		
DT		01-APR-1990 (Rel. 14, Last sequence update)		
DT		15-JUL-1999 (Rel. 38, Last annotation update)		
DE		Patacin class I precursor (Potato tuber protein).		
OS		Solanum tuberosum (Potato).		
OC		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;		
OC		lamiales; Solanales; Solanaceae; Solanum.		
OX		NCBI_TaxID=4113;		
RN		[1]		
RP		SEQUENCE FROM N.A.		
RC		STRAIN=cv. Superior;		
RX		MEDLINE=86226014; PubMed=3371664; DOI=10.1016/0378-1119(88)90577-X;		
RA		Mignery G.A., Pilkaard C.S., Park W.D.;		
RT		"Molecular characterization of the patacin multigene family of		
RT		potato."		
RL		Gene 62:27-44(1988).		
CC		-1- FUNCTION: Patacin may have a dual role as a somatic storage		
CC		protein and as an enzyme involved in host resistance. This tuber		
CC		protein represents approximately 40% of the total protein in		
CC		mature tubers.		
CC		-1- MISCELLANEOUS: There is strong evidence that patacin is a		
CC		lipolytic acyl hydrolase (LAH), an activity which is thought to be		
CC		involved in the response of tubers to pathogens.		
CC		-----		
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC		entities requires a license agreement (see http://www.isb-sib.ch/announce/		
CC		or send an email to license@isb-sib.ch).		
DR		EMBL; M18880; AAA33819.1; -		
DR		EMBL; M18883; AAA33831.1; -		
DR		PIR; A29810; A29810.		
DR		InterPro; IPRO02641; Patacin.		
DR		Pfam; PF01734; Patacin; 1.		
KW		Glycoprotein; Hydrolase; Multigene family; Signal; Storage protein.		
FT	CHAIN	1	23	Patacin class I.
FT	CARBOND	115	115	N-linked (GLCNAC... ) (Potential).
QO	SEQUENCE	386 AA;	7A20AFPAACD85229	CRC64;

Qy	144	QLEGMVTVLSIDGGGIRGIIIPATILFELEGLOEMDNNDARLADYDVIGTSTGGILT	203
Qy	144	QLEGMVTVLSIDGGGIRGIIIPATILFELEGLOEMDNNDARLADYDVIGTSTGGILT	203
Db	24	KLEEMVTVLSIDGGGIRGIIIPATILFELEGLOEVDDNNKARLADYDVIGTSTGGILT	83
Qy	204	AMISTENNRRPPAAAEIVPFPEHGPOIPNPSGQILGPKYDKKTYLMQVLQEKLGTRV	263
Db	84	AMITTPENNRRPPAAADIVPFPEHGPHIFNYSGSIIIGPYDKKTYLMQVLQEKLGTRV	143
Qy	264	HOALTEVVISFDIKTKMKPVIFPKSNANSPBELDAKKYDLSYSTPAAAPTEPPPHFYVNT	323
Db	144	HOALTEVAISSFDIKTKMKPVIFPKSNAKSPBELDAKKYDLCYSTPAAAPTEPPPHFYVNT	203
Qy	324	SNQDEYEFNLVDGAVATVADPALISISVATRLAQDKDPAPASIR	366
Db	204	SNQDIYEFNLVDGAVATVADGPPALLISVATRLAQDEDPAPESIK	246
RESULT 6			
PATO SOLUTU			
ID	PATO SOLUTU	STANDARD;	PRT; 386 AA.
AC	P07745;		
DT	01-AUG-1988	(Rel. 08, Created)	
DT	01-AUG-1988	(Rel. 08, Last sequence update)	
DT	01-APR-1990	(Rel. 14, Last annotation update)	
DE	Pataatin precursor (Potato tuber protein).		
OS	Solanum tuberosum (Potato)		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;		
OC	lamiales; Solanales; Solanaceae; Solanum.		
OX	NCBI_TaxID=4113;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Maris Piper 6094;		
RX	MEDLINE=86232596; PubMed=3714488;		
RA	Bevan M., Barker R., Goldsbrough A., Jarvis M., Kavanagh T.,		
RA	Iturriga G.;		
RT	"The structure and transcription start site of a major potato tuber		
RL	protein gene.";		
RL	Nucleic Acids Res. 14:4625-4638(1986).		
CC	-1- FUNCTION: Pataatin may have a dual role as a somatic storage		
CC	protein and as an enzyme involved in host resistance. This tuber		
CC	protein represents approximately 40% of the total protein in		
CC	mature tubers.		
CC	-1- MISCELLANEOUS: There is strong evidence that pataatin is a		
CC	lipolytic acyl hydrolase (LH), an activity which is thought to be		
CC	involved in the response of tubers to pathogens.		
CC	-----		
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		
CC	-----		
DR	EMBL; X03956; CAA27588.1; -		
DR	InterPro; IPR002641; Pataatin.		
KM	Pfam; PF01734; Pataatin; 1.		
DR	GlycoProtein; Hydrolase; Multigene family; Signal; Storage protein.		
FT	SIGNAL	1	23
FT	CHAIN	24	386
FT	CARBOHYD	115	115
SO	SEQUENCE	386 AA;	42490 MW; CF455970CCDB10B7 CRC64;
Query March	54.4%;	Score 10.14;	DB 1;
Best Local Similarity	88.3%;	Pred. No. 9;	1e-61;
Matches 196;	Conservative 13;	Mismatches 14;	Indels 0;
		Gaps 0;	

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QY 145 LGEWTVLISIDGGIGRIIPATILEFLEGOLOEMDNADARLADYDVIGSTGGLT 204
DB 25 LGEWTVLISIDGGIGRIIPATILEFLEGOLOEMDNADARLADYDVIGSTGGLT 84
QY 205 MISTPENNRPPAAAKEIVPFYFHEGPHIFNSGQILGPKYDKYLMQVLOEKLGETRV 264
DB 85 MISTPENNRPPAAAKEIVPFYFHEGPHIFNSGQILGPKYDKYLMQVLOEKLGETRV 144
QY 265 QALTEVVISFDDIKTKNPVIFTKSNLANSPELDARMYDISYSTAAAPYFPYFVNTS 324
DB 145 QALTEVVISFDDIKTKNPVIFTKSNLANSPELDARMYDISYSTAAAPYFPYFVNTS 204

QY 325 NGDEYFNLVDGAVATVADPALLISVATRLAQKDPAPASIR 366
DB 205 NGATYEFNLVDGAVATVADPALLISVATRLAQKDPAPASIR 246

RESULT 7
PAT2_SOLUTU STANDARD; PRT; 386 AA.
ID PAT2_SOLUTU STANDARD; PRT; 386 AA.
AC P15477;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Patatin B2 precursor (Potato tuber protein).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxId=4113;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Bintje;
RA Stiekema W.J., Heidekamp F., Dirkse W.G., van Beekun J., de Haan P.,
RA ten Bosch C., Louwerse J.D.;
RT "Molecular cloning and analysis of four potato tuber mRNAs.";
RL Plant Mol. Biol. 11:255-269(1988).
CC -1- FUNCTION: Patatin may have a dual role as a somatic storage
CC protein and as an enzyme involved in host resistance. This tuber
CC protein represents approximately 40% of the total protein in
CC mature tubers.
CC -1- MISCELLANEOUS: There is strong evidence that patatin is a
CC lipolytic acyl hydrolase (LH), an activity which is thought to be
CC involved in the response of tubers to pathogens.
CC
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CC -----
DR EMBL, X13178; CAJ31575.1; -.
DR PIR, S05592; S05592.
DR InterPro, IPR002641; Patatin.
DR Pfam, PF01734; Patatin.1.
KW Glycoprotein; Hydrolase; Multigene family; Signal; Storage protein.
FT CHAIN 1 23
FT SIGNAL 1 23
FT CATH 24 386 Patatin B2.
FT CARBOHYD 115 115 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 325 325 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 386 AA; 42612 MW; 5C0518B6A282405 CRC64;

Query Match 54.4%; Score 1014; DB 1; Length 386;
Best Local Similarity 88.3%; Pred. No. 1.5e-60;
Matches 197; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 144 QLGEMTVLISIDGGIGRIIPATILEFLEGOLOEMDNADARLADYDVIGSTGGLT 203
DB 24 KLEEMTVLISIDGGIGRIIPATILEFLEGOLOEMDNADARLADYDVIGSTGGLT 83
QY 204 AMISTPENNRPPAAAKEIVPFYFHEGPHIFNSGQILGPKYDKYLMQVLOEKLGETRV 263

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DB 84 AMITPENNRPPAAAKDVIPFYFHEGPHIFNYSGLLEGMIDGKLLQVLOEKLGETRV 143
QY 264 HQALTEVVISFDDIKTKNPVIFTKSNLANSPELDARMYDISYSTAAAPYFPYFVNT 323
DB 144 HQALTEVVISFDDIKTKNPVIFTKSNLANSPELDARMYDISYSTAAAPYFPYFVNT 203
QY 324 SNGDEYFNLVDGAVATVADPALLISVATRLAQKDPAPASIR 366
DB 204 SNGARYEFLNLVDGAVATVADPALLISVATRLAQKDPAPASIR 246

RESULT 8
Q41487 PRELIMINARY; PRT; 386 AA.
ID Q41487 PRELIMINARY; PRT; 386 AA.
AC Q41487; Q41473;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Patatin.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxId=4113;
RN [1]
RP SEQUENCE FROM N.A.
RA Kang M.J., Yang M.S.;
RT "Nucleotide Sequences of Class I Patatin cDNA from Potato Cultivated
RT in Korea.";
RL Plant Mol. Biol. 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RA Yang M.S.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL, Z27221; CAAB1735.1; -.
DR PIR, A23634; A23634.
DR PIR, T07592; T07592.
DR HSSP, QBLPW4; 10XW.
DR CO, GO:0003824; F:catalytic activity; IEA.
DR GO, GO:0045735; F:inucient reservoir activity; IEA.
DR InterPro, IPR002641; Patatin.
DR Pfam, PF01734; Patatin.1.
SQ SEQUENCE 386 AA; 42628 MW; A58E1DC9529BF0EF CRC64;

Query Match 53.8%; Score 1004; DB 2; Length 386;
Best Local Similarity 89.2%; Pred. No. 7e-60;
Matches 198; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 145 LGEWTVLISIDGGIGRIIPATILEFLEGOLOEMDNADARLADYDVIGSTGGLT 204
DB 25 LGEWTVLISIDGGIGRIIPATILEFLEGOLOEMDNADARLADYDVIGSTGGLT 84
QY 205 MISTPENNRPPAAAKEIVPFYFHEGPHIFNSGQILGPKYDKYLMQVLOEKLGETRV 264
DB 85 MISTPENNRPPAAAKEIVPFYFHEGPHIFNSGQILGPKYDKYLMQVLOEKLGETRV 144
QY 265 QALTEVVISFDDIKTKNPVIFTKSNLANSPELDARMYDISYSTAAAPYFPYFVNTS 324
DB 145 QALTEVVISFDDIKTKNPVIFTKSNLANSPELDARMYDISYSTAAAPYFPYFVNTS 204
QY 325 NGDEYFNLVDGAVATVADPALLISVATRLAQKDPAPASIR 366
DB 205 NGDKYEFLNLVDGAVATVADPALLISVATRLAQKDPAPASIR 246

RESULT 9
PAT1_SOLUTU STANDARD; PRT; 377 AA.
ID PAT1_SOLUTU STANDARD; PRT; 377 AA.
AC P15476;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE	Patatin B1 precursor (Potato tuber protein) (Fragment).
OS	Solanum tuberosum (Potato).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC	lamiales; Solanales; Solanaceae; Solanum.
OX	NCBI_TaxID=4113;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=cv. Bintje;
RA	Stiekema W.J., Heidekamp F., Dirkse W.G., van Beekun J., de Haan P.,
RT	ten Bosch C., Louwerse J.D.;
RA	"Molecular cloning and analysis of four potato tuber mRNAs";
PL	Plant Mol. Biol. 11:255-269(1988).
CC	-I- FUNCTION: Patatin may have a dual role as a somatic storage
CC	protein and as an enzyme involved in host resistance. This tuber
CC	protein represents approximately 40% of the total protein in
CC	mature tubers.
CC	-I- MISCELLANEOUS: There is strongly evidence that patatin is a
CC	lipolytic acyl hydrolase (LAH), an activity which is thought to be
CC	involved in the response of tubers to pathogens.
CC	-----
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CC	-----
DR	EMBL; X13179; CAA31576.1; .-
DR	PIR; S05593; S05593.
DR	IncePro; IPR002641; Patatin.
DR	Pfam; PF01734; Patatin; 1.
KW	Glycoprotein; Hydrolase; Multigene family; Signal; Storage protein.
FT	NON TER
FT	SIGNAL
FT	<1 14 Patatin B1.
FT	CHAIN 15 377 N-linked (GlcNAc...) (potential).
FT	CARBOHYD 106 106 A72307D49DD6AFC3 CRC64;
SQ	SEQUENCE 377 AA; 41615 MW; A72307D49DD6AFC3 CRC64;
Query Match	53.7%; Score 1002; DB 1; Length 377;
Best Local Similarity	87.0%; Pred. No. 9.2e-60;
Matches 194; Conservative 13; Mismatches 16; Indels 0; Gaps 0;	
OY	144 OLGHEVNTLSIDGGIRGIIPATILIEPLEGOLOEMDNNDARLADYPDVIGTGSTGGLLT 203
DB	: KLEEMVTYLSIDGGIKITPAIIIEFLEGOLQEVNNKDKARLADYFPVIGTSGGLLT 74
OY	204 AMISTPNENNRPPAAKEIVPFYFHGPQIFNPSCQILGPKYDGKYLMOVLQEKGETRV 263
DB	75 AMITTPENNNRPPAAKDIVPFFYFHGHFIHFYSGSIGFPRYDGKYLQLQVEKJGETRV 134
OY	264 HQALTEVVISSPDIKTNKPEVIFTSNLANSPELDKMWDISYSTAAPLPYPPHFVNT 323
DB	135 HQALTEVAISSFDIKTNKPVPFTKSNLAKSPELDKMWDTCSIAAPVIYPPHHFVHT 194
OY	324 SNGDEYEFNLDGAVALTADPALISIVATRLLAQKDPAFASIR 366
DB	195 SNGATYEPNLYDGVATVGDALLSLSTVATRLAQDPAFSSIK 237
RESULT 10	
ID	041467 PRELIMINARY; PRF; 386 AA.
AC	041467
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
OS	Potato patatin.
OS	Solanum tuberosum (Potato).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC	lamiales; Solanales; Solanaceae; Solanum.

OX NCBI\_TaxID=4113;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stiekema W.J., Heidekamp F., Dirkse W.G., van Beckum J., de Haan P.,  
RT ten Bosch C., Louwerse J.D.;  
RL "Molecular cloning and analysis of four potato tuber mRNAs";  
DR Plant Mol. Biol. 11:255-269(1988).  
EMBL; M21879; AAA33828.1; -  
PIR; B26017; B26017.  
DR HSSP; Q8LPW4; IOXW.  
DR GO; GO:0003824; F:catalytic activity; IEA.  
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.  
DR InterPro; IPR002641; Patatin.  
DR Pfam; PF01734; Patatin; 1.  
SO SEQUENCE 386 AA; 42626 MW; P3BA08CA08696CD5 CRC64;

Query Match 53.7%; Score 1002; DB 2; Length 386;  
Best Local Similarity 87.0%; Pred. No. 9.5e-60;  
Matches 194; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

OY 144 QLGEWTVVLSIDGGIGIIPATILFLEQLQEDMNNAARLADYEDVIGSTGILLT 203  
DB 24 KLSEWTVVLSIDGGIGIIPAILLEFLBEOQLQEDVNKCARLADYEDVIGSTGILLT 83

OY 204 AMISTPENNRPPAAAKEIVPEVEHEHGPJFNPSGOLLGPYDGYLMOVLQEKLGSTRV 263  
DB 84 AMITTPENNRPPAAAKDIVPFTEHGPHLFNYSGLFGPRDYKYLQVLQEKLGSTRV 143

OY 264 HQALTEVISFDIKTKNPVIFTKSNNANGSPELDARKMYDISYTAAPPTYEPHYFYNT 323  
DB 144 HQALTEVAISFDIKTKNPVIFTSNNLAKSPELDARKMYDISYTAAPPTYEPHYFYHT 203

OY 324 SNGDEYEFNVDGAATVADPALISIVATRLOAKDPAPASIR 366  
DB 204 SNGATYEFNLVDGVATGDPALISTSVATRILOEDPAFSISK 246

RESULT 11  
O8LSCI PRELIMINARY; PRT; 387 AA.

AC O8LSCI  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, last annotation update)  
DE Patatin storage protein.  
OS Solanum elaeagnace (Chaco potato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4108;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Huang J., Xie C.H., Liu J.;  
RT "Isolation and characterization of a cDNA of patatin, the major  
soluble protein of potato tuber.";  
RL Vestin. Sarat. Gos. Akad. Prava 1:65-70(2001).  
[2]  
RP SEQUENCE FROM N.A.  
RA Xie C.H., Huang J., Liu J.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
EMBL; AF498099; AAM21657.1; -  
DR HSSP; Q8LPW4; IOXW.  
DR GO; GO:0003824; F:catalytic activity; IEA.  
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.  
DR InterPro; IPR002641; Patatin.  
DR Pfam; PF01734; Patatin; 1.  
SO SEQUENCE 387 AA; 42756 MW; 12A46972BC2541B CRC64;

Query Match 53.4%; Score 996.5; DB 2; Length 387;  
Best Local Similarity 86.6%; Pred. No. 2.2e-59;  
Matches 194; Conservative 13; Mismatches 16; Indels 1; Gaps 1;

144 QLGEWTVVLSIDGGIGIIPATILFLEQLQEDMNNAARLADYEDVIGSTGILLT 203

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DB      24 KLEEMVTVLSIDGGIGIIPATILEFEQLOEMDNNAARLADYFDVIGSTGILTT 83
QY      204 AMISTENNRRPAAAKEIVPFYFEHGPQIFNPSG--ILGPKYDGKYLMOVLQEKLGETR 262
DB      84 AMITTENNRRPAAAKDVPFYFEHGPQIFNPSGRIFFPMTDGNLLOVLQEKLGETR 143
QY      263 VHQALTEVVISFDIKTKKPVIFTKSNLANSPEIDAKMYDISYSTAAPTYPFPHYFTVN 322
DB      144 VHQALTEVVISFDIKTKKPVIFTKSNLAKSPELDAMKDYICSTAAPMYFPPHYFTTH 203
QY      323 TNSGDEYEFNLVDGAVATVADPALISVATRLAQDPAFASIR 366
DB      204 TNSGDIYEFNLVDGAVATVADPALISVATRLAQEDPAFSSIK 247

RESULT 12
Q7DMC7 ID Q7DMC7 PRELIMINARY; PRT; 263 AA.
AC Q7DMC7;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
OS Nicotiana glauca (Common tobacco).
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93120883; PubMed=1477554;
RA Drews G.N., Beals T.P., Bui A.Q., Goldberg R.B.;
RT "Regional and cell-specific gene expression patterns during petal
development.";
RL Plant Cell 4:1383-1404 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RX Beals T.P., Goldberg R.B.;
RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
RL EMBL; U68483; AAB08427.1; -.
DB EMBL; U68483; AAB08427.1; -.
QY GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.
FT NON TER 263
SQ SEQUENCE 263 AA; 28225 MW; 66D617A7F0C7FBF3 CRC64;

Query Match 41.7%; Score 778.5; DB 2; Length 263;
Best Local Similarity 67.1%; Pred. No. 8e-45;
Matches 151; Conservative 31; Mismatches 36; Indels 7; Gaps 4;

QY 145 LGEWTVLSIDGGIGIIPATILEFEQLOEMDNNAARLADYFDVIGSTGILTTA 204
DB 25 VGSIAVTVLSIDGGIGIIPATVLSFLESQLOEDNNEDARLADYFDVIGSTGILTT 84
QY 205 MISTENNRRPAAAKEIVPFYFEHGPQIFNPSG--QILGPKYDGKYLMOVLQEKLGETR 261
DB 85 MISAPNEKRRPFAAKDVPFYFEHGPQIFNPSGRIFFPMTDGNLLOVLQEKLGETR 143
QY 262 RVHQALTEVVISFDIKTKKPVIFTKSNLANSPEIDAKMYDISYSTAAPTYPFPHYFTVN 321
DB 144 RVHQALTEVVISFDIKTKKPVIFTKSEIANSPEIDAKMSDICYSTAAPTYPFPHYFTVN 203
QY 322 NTSNGDEYEFNLVDGAVATVADPALISVATRLAQDPAFASIR 366
DB 204 DDKGNQHEFNLDGGVAV-NPALIAVSTYTK--SVDPVSASIK 245

RESULT 13
Q24152 ID Q24152 PRELIMINARY; PRT; 390 AA.
AC Q24152;

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DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Patatin homolog.
OS Nicotiana glauca (Common tobacco).
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93120883; PubMed=1477554;
RA Drews G.N., Beals T.P., Bui A.Q., Goldberg R.B.;
RT "Regional and cell-specific gene expression patterns during petal
development.";
RL Plant Cell 4:1383-1404 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RX Beals Thomas P., Goldberg R.B.;
RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
RL EMBL; U68484; AAB08428.1; -.
DR PIR; T03841; T03841.
DR HSSP; O8LPM4; 10XM.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.
SQ SEQUENCE 390 AA; 42499 MW; 9A70F5D9C85DB5F CRC64;

Query Match 41.7%; Score 778.5; DB 2; Length 390;
Best Local Similarity 67.1%; Pred. No. 1.4e-44;
Matches 151; Conservative 31; Mismatches 36; Indels 7; Gaps 4;

QY 145 LGEWTVLSIDGGIGIIPATILEFEQLOEMDNNAARLADYFDVIGSTGILTTA 204
DB 25 VGSIAVTVLSIDGGIGIIPATVLSFLESQLOEDNNEDARLADYFDVIGSTGILTT 84
QY 205 MISTENNRRPAAAKEIVPFYFEHGPQIFNPSG--QILGPKYDGKYLMOVLQEKLGETR 261
DB 85 MISAPNEKRRPFAAKDVPFYFEHGPQIFNPSGRIFFPMTDGNLLOVLQEKLGETR 143
QY 262 RVHQALTEVVISFDIKTKKPVIFTKSNLANSPEIDAKMYDISYSTAAPTYPFPHYFTVN 321
DB 144 RVHQALTEVVISFDIKTKKPVIFTKSEIANSPEIDAKMSDICYSTAAPTYPFPHYFTVN 203
QY 322 NTSNGDEYEFNLVDGAVATVADPALISVATRLAQDPAFASIR 366
DB 204 DDKGNQHEFNLDGGVAV-NPALIAVSTYTK--SVDPVSASIK 245

RESULT 14
Q8LBT5 ID Q8LBT5 PRELIMINARY; PRT; 383 AA.
AC Q8LBT5;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DE 01-OCT-2002 (T-EMBLrel. 25, Last annotation update)
OS Arabidopsis thaliana (Mouse-ear cress).
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC lamiales; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22088475; PubMed=12093376;
RA Haas B.U., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
annotation.";
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).
RN [2]
RP SEQUENCE FROM N.A.

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 8, 2005, 07:29:54 ; Search time 42 Seconds  
(without alignments)

650.513 Million cell updates/sec

Title: US-10-658-180-247

Perfect score: 1865

Sequence: 1 SLNYKKMLLSLGGTTSERF.....LSISVATRLAQDPAPASIR 366

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/PCUTS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1865	100.0	366	4	US-09-755-630B-247
2	1865	100.0	366	4	US-09-755-274-21
3	1865	100.0	389	4	US-09-755-630B-271
4	1865	100.0	389	4	US-09-755-274-33
5	1769	94.9	389	4	US-09-755-630B-275
6	1769	94.9	389	4	US-09-755-274-35
7	1753	94.0	366	4	US-09-755-630B-259
8	1753	94.0	366	4	US-09-755-274-27
9	1645	88.2	366	4	US-09-755-630B-251
10	1645	88.2	366	4	US-09-755-274-23
11	1544	82.8	366	4	US-09-755-630B-255
12	1544	82.8	366	4	US-09-755-274-25
13	1480	79.4	366	4	US-09-755-630B-263
14	1480	79.4	366	4	US-09-755-274-29
15	1139	61.1	367	4	US-09-755-630B-7
16	1139	61.1	367	4	US-09-755-274-41
17	1139	61.1	386	4	US-09-755-630B-1
18	1139	61.1	386	4	US-09-755-630B-265
19	1139	61.1	386	4	US-09-755-630B-286
20	1139	61.1	386	4	US-09-755-274-1
21	1139	61.1	386	4	US-09-755-274-31
22	1139	61.1	386	4	US-09-755-274-39
23	1139	61.1	452	4	US-09-755-630B-6
24	1139	61.1	452	4	US-09-755-274-40
25	1030.5	55.3	383	1	US-07-936-163-4
26	1019	54.6	386	4	US-09-755-630B-279
27	1019	54.6	386	4	US-09-755-274-6

28	1017	54.5	386	4	US-09-755-630B-278	Sequence 278, App
29	1017	54.5	386	4	US-09-755-274-5	Sequence 5, Appl1
30	1014	54.4	381	1	US-07-936-163-3	Sequence 3, Appl1
31	1014	54.4	386	4	US-09-755-630B-282	Sequence 282, App
32	1014	54.4	386	4	US-09-755-274-4	Sequence 4, Appl1
33	1013	54.3	364	4	US-09-755-630B-281	Sequence 281, App
34	1013	54.3	364	4	US-09-755-274-3	Sequence 3, Appl1
35	1001.5	53.7	365	4	US-09-755-630B-280	Sequence 280, App
36	1001.5	53.7	365	4	US-09-755-274-2	Sequence 2, Appl1
37	528.5	28.3	408	3	US-09-074-912-2	Sequence 2, Appl1
38	528.5	28.3	408	3	US-09-074-912-4	Sequence 4, Appl1
39	528.5	28.3	408	3	US-09-290-136-2	Sequence 2, Appl1
40	528.5	28.3	408	3	US-09-290-136-4	Sequence 4, Appl1
41	528.5	28.3	408	4	US-09-755-630B-287	Sequence 287, App
42	528.5	28.3	408	4	US-09-755-274-7	Sequence 7, Appl1
43	523	28.0	410	4	US-09-755-630B-290	Sequence 290, App
44	523	28.0	410	4	US-09-755-274-10	Sequence 10, Appl1
45	520	27.9	337	4	US-09-755-630B-293	Sequence 293, App

#### ALIGNMENTS

```
RESULT 1
US-09-755-630B-247
; Sequence 247, Application US/09755630B
; Patent No. 6639054
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCWHIRTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTATIONS
; FILE REFERENCE: 11899.0217.NPUS00 (WO/0217)
; CURRENT APPLICATION NUMBER: US/09/755,630B
; PRIOR APPLICATION NUMBER: US 60/174,669
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630B-247

Query Match      100.0%; Score 1865; DB 4; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.6e-169;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLNYKKMLLSLGGTTSERFDTYTAKEATWAVHMLVIQKMTDAASSYMTDYLYSTA 60
DB      1 SLNYKKMLLSLGGTTSERFDTYTAKEATWAVHMLVIQKMTDAASSYMTDYLYSTA 60

QY      61 FOALDSKNNTLYRQENALTTTTEMDASANNELLVQVENNLKKRVSNDNETYEAL 120
DB      61 FOALDSKNNTLYRQENALTTTTEMDASANNELLVQVENNLKKRVSNDNETYEAL 120

QY      61 FOALDSKNNTLYRQENALTTTTEMDASANNELLVQVENNLKKRVSNDNETYEAL 120
DB      61 FOALDSKNNTLYRQENALTTTTEMDASANNELLVQVENNLKKRVSNDNETYEAL 120

QY      121 KRFAKLSDRRKKLRANKASVGPQLGEMTVLSDGGGIGITIPATLLEFLBQLOQMDN 180
DB      121 KRFAKLSDRRKKLRANKASVGPQLGEMTVLSDGGGIGITIPATLLEFLBQLOQMDN 180

QY      181 NADARLADYDVIGTSTGGLTAMISTPENNNRPPAAAEIVPFYEHGPQIFNPGOI 240
DB      181 NADARLADYDVIGTSTGGLTAMISTPENNNRPPAAAEIVPFYEHGPQIFNPGOI 240

QY      241 LGRPYDKYIMOVLOEGLGSTRVHQALETYVSSFDIKTKKPVITFKSNLANSPELDAM 300
DB      241 LGRPYDKYIMOVLOEGLGSTRVHQALETYVSSFDIKTKKPVITFKSNLANSPELDAM 300

QY      301 YDISYTAAPATYFPFHYFVTNTNSGDEYFNLVDGAVATVADPALISVATRLAQKDP 360
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DB 301 YDISYSTAAAPTYFPFPHYFTVNTNSNGDEYEFNLVDGAVALTVADPALLISVATRLAQKDP 360  
QY 361 AFASIR 366  
DB 361 AFASIR 366

## RESULT 2

US-09-755-274-21  
; Sequence 21, Application US/09755274  
; Patent No. 6657046  
; GENERAL INFORMATION:  
; APPLICANT: Alibhai, Murtaza  
; APPLICANT: Rydel, Timothy  
; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases  
; FILE REFERENCE: 38-21 (51842)B  
; CURRENT APPLICATION NUMBER: US/09/755,274  
; CURRENT FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 21  
; LENGTH: 366  
; TYPE: PRT  
; ORGANISM: synthetic  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: (1)..(366)  
; OTHER INFORMATION: Permutin protein encoded from pMON37402 sequence  
US-09-755-274-21

Query Match 100.0%; Score 1865; DB 4; Length 366;  
Best Local Similarity 100.0%; Pred. No. 1.6e-169;  
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSIGTGTSEFDKTYTAKEATWTAHVHMLVIOKMTDAASSYMTDYILSTA 60  
DB 1 SLNYKKMLLSIGTGTSEFDKTYTAKEATWTAHVHMLVIOKMTDAASSYMTDYILSTA 60  
QY 61 FOALDSKNNTLRQVENALGTTTMDASBANNELLVQVGENLLKKPVSEDNPEYEEAL 120  
DB 61 FOALDSKNNTLRQVENALGTTTMDASBANNELLVQVGENLLKKPVSEDNPEYEEAL 120  
QY 121 KRFKLLSDRKKLRANKASYGPGQLGEMTVLSIDGGIRGIIPATLLEFLBQLOEMDN 180  
DB 121 KRFKLLSDRKKLRANKASYGPGQLGEMTVLSIDGGIRGIIPATLLEFLBQLOEMDN 180  
QY 181 NADARLADYFDVIGTSTGGLTAMISTPNENNRPPAAKEIVPFYFEGHQPQIFNPSGQI 240  
DB 181 NADARLADYFDVIGTSTGGLTAMISTPNENNRPPAAKEIVPFYFEGHQPQIFNPSGQI 240  
QY 241 LGPKYDGKYLMOVLQEKLGSTRVHQAALTEVVISFDIKTKNPVIFTKSNLANSPELDAM 300  
DB 241 LGPKYDGKYLMOVLQEKLGSTRVHQAALTEVVISFDIKTKNPVIFTKSNLANSPELDAM 300  
QY 301 YDISYSTAAAPTYFPFPHYFTVNTNSNGDEYEFNLVDGAVALTVADPALLISVATRLAQKDP 360  
DB 301 YDISYSTAAAPTYFPFPHYFTVNTNSNGDEYEFNLVDGAVALTVADPALLISVATRLAQKDP 360  
QY 361 AFASIR 366  
DB 361 AFASIR 366

## RESULT 3

US-09-755-630B-271  
; Sequence 271, Application US/09755630B  
; Patent No. 6639054  
; GENERAL INFORMATION:  
; APPLICANT: Alibhai, Murtaza F.  
; APPLICANT: ASTWOOD, JAMES D.  
; APPLICANT: SAMPSON, HUGH A.  
; APPLICANT: MCMHENTER, CHARLES A.

; TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTINS  
; FILE REFERENCE: 11899.0217.NPUS00 (KOB1217)  
; CURRENT APPLICATION NUMBER: US/09/755,630B  
; CURRENT FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 60/174,669  
; PRIOR FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 295  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 271  
; LENGTH: 389  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic polypeptide  
US-09-755-630B-271

Query Match 100.0%; Score 1865; DB 4; Length 389;  
Best Local Similarity 100.0%; Pred. No. 1.7e-169;  
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSIGTGTSEFDKTYTAKEATWTAHVHMLVIOKMTDAASSYMTDYILSTA 60  
DB 24 SLNYKKMLLSIGTGTSEFDKTYTAKEATWTAHVHMLVIOKMTDAASSYMTDYILSTA 83  
QY 61 FOALDSKNNTLRQVENALGTTTMDASBANNELLVQVGENLLKKPVSEDNPEYEEAL 120  
DB 84 FOALDSKNNTLRQVENALGTTTMDASBANNELLVQVGENLLKKPVSEDNPEYEEAL 143  
QY 121 KRFKLLSDRKKLRANKASYGPGQLGEMTVLSIDGGIRGIIPATLLEFLBQLOEMDN 180  
DB 144 KRFKLLSDRKKLRANKASYGPGQLGEMTVLSIDGGIRGIIPATLLEFLBQLOEMDN 203  
QY 181 NADARLADYFDVIGTSTGGLTAMISTPNENNRPPAAKEIVPFYFEGHQPQIFNPSGQI 240  
DB 204 NADARLADYFDVIGTSTGGLTAMISTPNENNRPPAAKEIVPFYFEGHQPQIFNPSGQI 263  
QY 241 LGPKYDGKYLMOVLQEKLGSTRVHQAALTEVVISFDIKTKNPVIFTKSNLANSPELDAM 300  
DB 264 LGPKYDGKYLMOVLQEKLGSTRVHQAALTEVVISFDIKTKNPVIFTKSNLANSPELDAM 323  
QY 301 YDISYSTAAAPTYFPFPHYFTVNTNSNGDEYEFNLVDGAVALTVADPALLISVATRLAQKDP 360  
DB 324 YDISYSTAAAPTYFPFPHYFTVNTNSNGDEYEFNLVDGAVALTVADPALLISVATRLAQKDP 383  
QY 361 AFASIR 366  
DB 384 AFASIR 389

## RESULT 4

US-09-755-274-33  
; Sequence 33, Application US/09755274  
; Patent No. 6657046  
; GENERAL INFORMATION:  
; APPLICANT: Alibhai, Murtaza  
; APPLICANT: Rydel, Timothy  
; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases  
; FILE REFERENCE: 38-21 (51842)B  
; CURRENT APPLICATION NUMBER: US/09/755,274  
; CURRENT FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 33  
; LENGTH: 389  
; TYPE: PRT  
; ORGANISM: synthetic  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: (1)..(389)  
; OTHER INFORMATION: Permutin protein encoded by pMON40703 sequence  
US-09-755-274-33

Query Match 100.0%; Score 1865; DB 4; Length 389;

Best Local Similarity 100.0%; Pred. No. 1.7e-169;  
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 SINYKMLLSIGTSTSEFDKTYTAKEATWTAVHMMVLVIQMTDAASVMTDYLLSTA 60
DB 24 SINYKMLLSIGTSTSEFDKTYTAKEATWTAVHMMVLVIQMTDAASVMTDYLLSTA 83
QY 61 FQALDSKNNYLRVOENALIGTTEMDDASEANMELLVQGENLLKKPVSEDPETEYEAAL 120
DB 84 FQALDSKNNYLRVOENALIGTTEMDDASEANMELLVQGENLLKKPVSEDPETEYEAAL 143
QY 121 KRPAPKLSDRKKLRANKASYGPGQIGEMVTVLISIDGGIRGIIIPATILFELGQLOEMDN 180
DB 144 KRPAPKLSDRKKLRANKASYGPGQIGEMVTVLISIDGGIRGIIIPATILFELGQLOEMDN 203
QY 181 NADARLADYFDVIGTSTGGLLTAMISTPENNNRPAAAKEIVPFYFEGHQPQIFNPSGQI 240
DB 204 NADARLADYFDVIGTSTGGLLTAMISTPENNNRPAAAKEIVPFYFEGHQPQIFNPSGQI 263
QY 241 LQPKYDGLMOVLQEKGETRVHQALTEVVISPDIKTKKPVIFTKSNLANSPELDACKM 300
DB 264 LQPKYDGLMOVLQEKGETRVHQALTEVVISPDIKTKKPVIFTKSNLANSPELDACKM 323
QY 301 YDISYSTAAAPTYPPHYFVNTNSNGDEYEFNLVDGAVATVADPALLISVATRLAQKXP 360
DB 324 YDISYSTAAAPTYPPHYFVNTNSNGDEYEFNLVDGAVATVADPALLISVATRLAQKXP 383
QY 361 APASIR 366
DB 384 APASIR 389
```

## RESULT 5

US-09-755-630B-275  
Sequence 275, Application US/09755630B  
Patent No. 6639054

GENERAL INFORMATION:  
APPLICANT: ALIBHAI, MURTAZA F.  
APPLICANT: ASTWOOD, JAMES D.  
APPLICANT: SAMPSON, HUGH A.  
APPLICANT: MCWERTER, CHARLES A.  
TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTAINS  
FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)  
CURRENT APPLICATION NUMBER: US/09/755,630B  
CURRENT FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: US 60/174,669  
PRIOR FILING DATE: 2000-01-06  
NUMBER OF SEQ ID NOS: 295  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 275  
LENGTH: 389  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic polypeptide  
US-09-755-630B-275

Query Match 94.9%; Score 1769; DB 4; Length 389;  
Best Local Similarity 96.7%; Pred. No. 2.5e-160;  
Matches 348; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

```
QY 7 MLLLSIGTSTSEFDKTYTAKEATWTAVHMMVLVIQMTDAASVMTDYLLSTAFAQLDS 66
DB 8 LILIFMILATTSSTFATYTAKEATWTAVHMMVLVIQMTDAASVMTDYLLSTAFAQLDS 67
QY 67 KNNYLVRVOENALIGTTEMDDASEANMELLVQGENLLKKPVSEDPETEYEAALKRFAPKL 126
DB 68 KNNYLVRVOENALIGTTEMDDASEANMELLVQGENLLKKPVSEDPETEYEAALKRFAPKL 127
QY 127 LSDRKKLRANKASYGPGQIGEMVTVLISIDGGIRGIIIPATILFELGQLOEMDNADARL 186
DB 128 LSDRKKLRANKASYGPGQIGEMVTVLISIDGGIRGIIIPATILFELGQLOEMDNADARL 187
```

QY 187 ADYFDVIGTSTGGLLTAMISTPENNNRPAAAKEIVPFYFEGHQPQIFNPSGQILGPXYD 246  
DB 188 ADYFDVIGTSTGGLLTAMISTPENNNRPAAAKEIVPFYFEGHQPQIFNPSGQILGPXYD 247

```
QY 247 GKTIQVLOEKGETRVHQALTEVVISPDIKTKKPVIFTKSNLANSPELDACKYDYSYS 306
DB 248 GKTIQVLOEKGETRVHQALTEVVISPDIKTKKPVIFTKSNLANSPELDACKYDYSYS 307
QY 307 TAAAPTYPPHYFVNTNSNGDEYEFNLVDGAVATVADPALLISVATRLAQKXPAPASIR 366
DB 308 TAAAPTYPPHYFVNTNSNGDEYEFNLVDGAVATVADPALLISVATRLAQKXPAPASIR 367
```

## RESULT 6

US-09-755-274-35

Sequence 35, Application US/09755274  
Patent No. 6657046  
GENERAL INFORMATION:  
APPLICANT: Alibhai, Murtaza  
APPLICANT: Rydel, Timothy  
TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases  
FILE REFERENCE: 38-21 (51842)B  
CURRENT APPLICATION NUMBER: US/09/755,274  
CURRENT FILING DATE: 2001-01-05  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 35  
LENGTH: 389  
TYPE: PRT  
ORGANISM: synthetic  
FEATURE:  
NAME/KEY: Protein  
LOCATION: (1)..(389)  
OTHER INFORMATION: Permutain protein encoded by pMON40705  
US-09-755-274-35

Query Match 94.9%; Score 1769; DB 4; Length 389;  
Best Local Similarity 96.7%; Pred. No. 2.5e-160;  
Matches 348; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

```
QY 7 MLLLSIGTSTSEFDKTYTAKEATWTAVHMMVLVIQMTDAASVMTDYLLSTAFAQLDS 66
DB 8 LILIFMILATTSSTFATYTAKEATWTAVHMMVLVIQMTDAASVMTDYLLSTAFAQLDS 67
QY 67 KNNYLVRVOENALIGTTEMDDASEANMELLVQGENLLKKPVSEDPETEYEAALKRFAPKL 126
DB 68 KNNYLVRVOENALIGTTEMDDASEANMELLVQGENLLKKPVSEDPETEYEAALKRFAPKL 127
QY 127 LSDRKKLRANKASYGPGQIGEMVTVLISIDGGIRGIIIPATILFELGQLOEMDNADARL 186
DB 128 LSDRKKLRANKASYGPGQIGEMVTVLISIDGGIRGIIIPATILFELGQLOEMDNADARL 187
QY 187 ADYFDVIGTSTGGLLTAMISTPENNNRPAAAKEIVPFYFEGHQPQIFNPSGQILGPXYD 246
DB 188 ADYFDVIGTSTGGLLTAMISTPENNNRPAAAKEIVPFYFEGHQPQIFNPSGQILGPXYD 247
QY 247 GKTIQVLOEKGETRVHQALTEVVISPDIKTKKPVIFTKSNLANSPELDACKYDYSYS 306
DB 248 GKTIQVLOEKGETRVHQALTEVVISPDIKTKKPVIFTKSNLANSPELDACKYDYSYS 307
QY 307 TAAAPTYPPHYFVNTNSNGDEYEFNLVDGAVATVADPALLISVATRLAQKXPAPASIR 366
DB 308 TAAAPTYPPHYFVNTNSNGDEYEFNLVDGAVATVADPALLISVATRLAQKXPAPASIR 367
```

## RESULT 7

US-09-755-630B-259  
Sequence 259, Application US/09755630B  
Patent No. 6639054

GENERAL INFORMATION:  
APPLICANT: ALIBHAI, MURTAZA F.  
APPLICANT: ASTWOOD, JAMES D.  
APPLICANT: SAMPSON, HUGH A.

```

; APPLICANT: McHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTEDS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755,630B
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 259
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630B-259

```

```

Query Match          94.0%; Score 1753; DB 4; Length 366;
Best Local Similarity 99.7%; Pred. No. 7.7e-159;
Matches 343; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 23 TYTAKAAATWTAHMMVLVIQKMTDAASSYMTDYLLSTAFOALDSKNNYLKVOENALTGTT 82
DB 1 TYTAKAAATWTAHMMVLVIQKMTDAASSYMTDYLLSTAFOALDSKNNYLKVOENALTGTT 60

QY 83 TEMDDASEANMELLVOGENLLKKPVSEDPETYEALRFAKLSDRKKLRANKASYGP 142
DB 61 TEMDDASEANMELLVOGENLLKKPVSEDPETYEALRFAKLSDRKKLRANKASYGP 120

QY 143 GOLGEWTVLSTIDGGIRGIIIPATILIEPLEGOLQEMDNADRLADYFVIGTSTGGIL 202
DB 121 GOLGEWTVLSTIDGGIRGIIIPATILIEPLEGOLQEMDNADRLADYFVIGTSTGGIL 180

QY 203 TMIISTPNNRNPFAAKEIVPFYFHEGPOIFNPSSQILGPKYDGKYLMOVLQEKLGTR 262
DB 181 TMIISTPNNRNPFAAKEIVPFYFHEGPOIFNPSSQILGPKYDGKYLMOVLQEKLGTR 240

QY 263 VHQALTEVVISFDITKPKVIFTKSNLANSPELDKMDISYSTAAAPTFPPHYFVTN 322
DB 241 VHQALTEVVISFDITKPKVIFTKSNLANSPELDKMDISYSTAAAPTFPPHYFVTN 300

QY 323 TSNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 366
DB 301 TSNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 344

```

```

RESULT 8
US-09-755-274-27
; Sequence 27, Application US/09755274
; Patent No. 6657046
; GENERAL INFORMATION:
; APPLICANT: Alibhai, Murtaza
; APPLICANT: Rydel, Timothy
; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases
; FILE REFERENCE: 38-21 (51842)B
; CURRENT APPLICATION NUMBER: US/09/755,274
; CURRENT FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 366
; TYPE: PRT
; ORGANISM: synthetic
; FEATURE:
; NAME/KEY: Protein
; LOCATION: (1)..(366)
; OTHER INFORMATION: Permutated protein encoded by pMON37407 sequence
US-09-755-274-27

```

```

Query Match          94.0%; Score 1753; DB 4; Length 366;
Best Local Similarity 99.7%; Pred. No. 7.7e-159;
Matches 343; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 23 TYTAKAAATWTAHMMVLVIQKMTDAASSYMTDYLLSTAFOALDSKNNYLKVOENALTGTT 82
DB 1 TYTAKAAATWTAHMMVLVIQKMTDAASSYMTDYLLSTAFOALDSKNNYLKVOENALTGTT 60

QY 83 TEMDDASEANMELLVOGENLLKKPVSEDPETYEALRFAKLSDRKKLRANKASYGP 142
DB 61 TEMDDASEANMELLVOGENLLKKPVSEDPETYEALRFAKLSDRKKLRANKASYGP 120

QY 143 GOLGEWTVLSTIDGGIRGIIIPATILIEPLEGOLQEMDNADRLADYFVIGTSTGGIL 202
DB 121 GOLGEWTVLSTIDGGIRGIIIPATILIEPLEGOLQEMDNADRLADYFVIGTSTGGIL 180

QY 203 TMIISTPNNRNPFAAKEIVPFYFHEGPOIFNPSSQILGPKYDGKYLMOVLQEKLGTR 262
DB 181 TMIISTPNNRNPFAAKEIVPFYFHEGPOIFNPSSQILGPKYDGKYLMOVLQEKLGTR 240

QY 263 VHQALTEVVISFDITKPKVIFTKSNLANSPELDKMDISYSTAAAPTFPPHYFVTN 322
DB 241 VHQALTEVVISFDITKPKVIFTKSNLANSPELDKMDISYSTAAAPTFPPHYFVTN 300

QY 323 TSNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 366
DB 301 TSNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 344

```

```

RESULT 9
US-09-755-630B-251
; Sequence 251, Application US/09755630B
; Patent No. 6639054
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: SAMSON, HUGH A.
; APPLICANT: McHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTEDS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755,630B
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 251
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630B-251

```

```

Query Match          88.2%; Score 1645; DB 4; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.6e-146;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 SLNYKKMLLSIGTGTSTSPDKTYTAKAAATWTAHMMVLVIQKMTDAASSYMTDYLLSTA 60
DB 46 SLNYKKMLLSIGTGTSTSPDKTYTAKAAATWTAHMMVLVIQKMTDAASSYMTDYLLSTA 105

QY 61 FOALDSKNNYLKVOENALTGTTTEMDDASEANMELLVOGENLLKKPVSEDPETYEAL 120
DB 106 FOALDSKNNYLKVOENALTGTTTEMDDASEANMELLVOGENLLKKPVSEDPETYEAL 165

QY 121 KRPAKLSDRKKLRANKASYGPQOLGEWTVLSTIDGGIRGIIIPATILIEPLEGOLQEMDN 180
DB 166 KRPAKLSDRKKLRANKASYGPQOLGEWTVLSTIDGGIRGIIIPATILIEPLEGOLQEMDN 225

QY 181 NADARLADYFVIGTSTGGILTAMISTPNNRNPFAAKEIVPFYFHEGPOIFNPSSQI 240
DB 226 NADARLADYFVIGTSTGGILTAMISTPNNRNPFAAKEIVPFYFHEGPOIFNPSSQI 285

QY 241 LGGKYDGKYLMOVLQEKLGTRVHQALTEVVISFDITKPKVIFTKSNLANSPELDKMD 300
DB 286 LGGKYDGKYLMOVLQEKLGTRVHQALTEVVISFDITKPKVIFTKSNLANSPELDKMD 345

```

QY 301 YDISYSTAAAPTYFPPHYFT 321  
DB 346 YDISYSTAAAPTYFPPHYFT 366

## RESULT 10

US-09-755-274-23  
Sequence 23, Application US/09755274

Patent No. 6657046

GENERAL INFORMATION:

APPLICANT: Alibhai, Murtaza

APPLICANT: Rydel, Timothy

TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases

FILE REFERENCE: 38-21 (51842)B

CURRENT APPLICATION NUMBER: US/09/755,274

CURRENT FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin version 3.0

SEQ ID NO 23

LENGTH: 366

TYPE: PRT

ORGANISM: synthetic

FEATURE:

NAME/KEY: Protein

LOCATION: (1)..(366)

OTHER INFORMATION: Permutin protein encoded by pMON37405 sequence

US-09-755-274-23

Query Match 88.2%; Score 1645; DB 4; Length 366;

Best Local Similarity 100.0%; Pred. No. 1.6e-148;

Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSLGTGTTSEPDKTYTAKAATWAVHMLVIQKWTDAASSYMTDYISTA 60

DB 46 SLNYKKMLLSLGTGTTSEPDKTYTAKAATWAVHMLVIQKWTDAASSYMTDYISTA 105

QY 61 FOALDSKNNTLRVOENALTGTTEMDASEANMELLVQVGENLLKRVSEDNPEYREAL 120

DB 106 FOALDSKNNTLRVOENALTGTTEMDASEANMELLVQVGENLLKRVSEDNPEYREAL 165

QY 121 KRPAKLISDRKRLRANKASYGPGQIGEMTVLISIDGGIRIGIIPATLLEFLEGOLOEMDN 180

DB 166 KRPAKLISDRKRLRANKASYGPGQIGEMTVLISIDGGIRIGIIPATLLEFLEGOLOEMDN 225

QY 181 NADARLADYFDVIGSTGGLTAMISTPENNNRPFAAAEIVPFYFHEGPQIFNPSGOI 240

DB 226 NADARLADYFDVIGSTGGLTAMISTPENNNRPFAAAEIVPFYFHEGPQIFNPSGOI 285

QY 241 LGPKYDGKYLMOVLQEKLGSTRVHQALTEVVISFDIKTKNPVIFTKSNLANSPELDAM 300

DB 286 LGPKYDGKYLMOVLQEKLGSTRVHQALTEVVISFDIKTKNPVIFTKSNLANSPELDAM 345

QY 301 YDISYSTAAAPTYFPPHYFT 321

DB 346 YDISYSTAAAPTYFPPHYFT 366

## RESULT 11

US-09-755-630B-255

Sequence 255, Application US/09755630B

Patent No. 6639054

GENERAL INFORMATION:

APPLICANT: Alibhai, Murtaza F.

APPLICANT: ASTWOOD, JAMES D.

APPLICANT: SAMPSON, HUGH A.

APPLICANT: MCHESTER, CHARLES A.

TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTINS

FILE REFERENCE: 11899 0217.NPUS00 (MOBT217)

CURRENT APPLICATION NUMBER: US/09/755,630B

CURRENT FILING DATE: 2001-01-05

PRIOR APPLICATION NUMBER: US 60/174,669

PRIOR FILING DATE: 2000-01-06

NUMBER OF SEQ ID NOS: 295  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 255  
LENGTH: 366

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic polypeptide

US-09-755-630B-255

Query Match 82.8%; Score 1544; DB 4; Length 366;

Best Local Similarity 100.0%; Pred. No. 6.9e-139;

Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSLGTGTTSEPDKTYTAKAATWAVHMLVIQKWTDAASSYMTDYISTA 60

DB 64 SLNYKKMLLSLGTGTTSEPDKTYTAKAATWAVHMLVIQKWTDAASSYMTDYISTA 123

QY 61 FOALDSKNNTLRVOENALTGTTEMDASEANMELLVQVGENLLKRVSEDNPEYREAL 120

DB 124 FOALDSKNNTLRVOENALTGTTEMDASEANMELLVQVGENLLKRVSEDNPEYREAL 183

QY 121 KRPAKLISDRKRLRANKASYGPGQIGEMTVLISIDGGIRIGIIPATLLEFLEGOLOEMDN 180

DB 184 KRPAKLISDRKRLRANKASYGPGQIGEMTVLISIDGGIRIGIIPATLLEFLEGOLOEMDN 243

QY 181 NADARLADYFDVIGSTGGLTAMISTPENNNRPFAAAEIVPFYFHEGPQIFNPSGOI 240

DB 244 NADARLADYFDVIGSTGGLTAMISTPENNNRPFAAAEIVPFYFHEGPQIFNPSGOI 303

QY 241 LGPKYDGKYLMOVLQEKLGSTRVHQALTEVVISFDIKTKNPVIFTKSNLANSPELDAM 300

DB 304 LGPKYDGKYLMOVLQEKLGSTRVHQALTEVVISFDIKTKNPVIFTKSNLANSPELDAM 363

QY 301 YDI 303

DB 364 YDI 366

## RESULT 12

US-09-755-274-25

Sequence 25, Application US/09755274

Patent No. 6657046

GENERAL INFORMATION:

APPLICANT: Alibhai, Murtaza

APPLICANT: Rydel, Timothy

TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases

FILE REFERENCE: 38-21 (51842)B

CURRENT APPLICATION NUMBER: US/09/755,274

CURRENT FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin version 3.0

SEQ ID NO 25

LENGTH: 366

TYPE: PRT

ORGANISM: synthetic

FEATURE:

NAME/KEY: Protein

LOCATION: (1)..(366)

OTHER INFORMATION: Permutin protein encoded by pMON37406

US-09-755-274-25

Query Match 82.8%; Score 1544; DB 4; Length 366;

Best Local Similarity 100.0%; Pred. No. 6.9e-139;

Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSLGTGTTSEPDKTYTAKAATWAVHMLVIQKWTDAASSYMTDYISTA 60

DB 64 SLNYKKMLLSLGTGTTSEPDKTYTAKAATWAVHMLVIQKWTDAASSYMTDYISTA 123

QY 61 FOALDSKNNTLRVOENALTGTTEMDASEANMELLVQVGENLLKRVSEDNPEYREAL 120

DB 124 FOALDSKNNTLRVOENALTGTTEMDASEANMELLVQVGENLLKRVSEDNPEYREAL 183

QY	DB	QY	DB
121	184	301	364
KRPAKLSIRKTLRAKAKAYGQJGEMWTYVLSIDGGIRIGIIPATILFLEBQJQJMDN	KRPAKLSIRKTLRAKAKASYGPQJGEMWTYVLSIDGGIRIGIIPATILFLEBQJQJMDN	YDI 303	YDI 366
181	244		
NADARLADYFDVIGSTSGLLTAMISPTENNRRPFAAKEIVPPEFHHQJFNPSSQI	NADARLADYFDVIGSTSGLLTAMISPTENNRRPFAAKEIVPPEFHHQJFNPSSQI		
241	304		
LGKRYGKTIQVLOJRKJGRTVHQALTEVVISSPDITKNPVIFTKSNLANSBELDARK	LGKRYGKTIQVLOJRKJGRTVHQALTEVVISSPDITKNPVIFTKSNLANSBELDARK		
301	364		
YDI 303	YDI 366		

```

RESULT 13
US-09-755-6308-263
; Sequence 263. Application US/09755630B
; Patent No. 6639054
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPOON, HUGH A.
; APPLICANT: MCWHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMOXTEINS
; FILE REFERENCE: 11899,0217.NFUS00 (MOB7217)
; CURRENT APPLICATION NUMBER: US/09/755,630B
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 263
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
; US-09-755-6308-263

```

```

? APPLICANT: Alibhai, Murtaza
? APPLICANT: Rygel, Timothy
? TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolase
? FILE REFERENCE: 38-21 (51842)B
? CURRENT APPLICATION NUMBER: US/09/755,274
? CURRENT FILING DATE: 2001-01-05
? NUMBER OF SEQ ID NOS: 60
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 29
? LENGTH: 366
? TYPE: PRT
? ORGANISM: synthetic
? FEATURE:
? NAME/KEY: Protein
? LOCATION: (1)..(366)
? OTHER INFORMATION: Permuterin protein encoded by pMON37408
US-09-755-274-29

```

	Query March	79.4%;	Score 1480;	DB 4;	Length 366;
	Best Local Similarity	100.0%;	Pred. No. 8,9e-133;		
	Matches 291;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	76 NATGTTTMDASEANELLVQVEENLLKKPVSSDNPEYEEALKRPAKLISDRKKLRA	135			
Db	1 NATGGTTTMDASEANELLVQVEENLLKKPVSSDNPEYEEALKRPAKLISDRKKLRA	60			
QY	136 NKASVGPQQLGEMTVLVSIDGGGRGIIIPATLLELEQLOMDNNADARLADYEDVIGG	195			
Db	61 NKASVGPQQLGEMTVLVSIDGGGRGIIIPATLLELEQLOMDNNADARLADYEDVIGG	120			
QY	196 TSTGGLLTAMISTENENRRPFAAAKEIVPFYFEHSPQIFNBSGQILGPKYDGYLMQVLQ	255			
Db	121 TSTGGLLTAMISTENENRRPFAAAKEIVPFYFEHSPQIFNBSGQILGPKYDGYLMQVLQ	180			
QY	256 EKLGETRVHQAALTEVVISSPDIKTNKPVIFTKSNLANSPELDARKMYDISYSTAAAPTYFP	315			
Db	181 EKLGETRVHQAALTEVVISSPDIKTNKPVIFTKSNLANSPELDARKMYDISYSTAAAPTYFP	240			
QY	316 PHYEVYTNNSNDEYEFNLVDGAVLVAVAPALSTISVATRLAQKDPAPASIR	366			
Db	241 PHYVYTNNSNDEYEFNLVDGAVLVAVAPALSTISVATRLAQKDPAPASIR	291			

RESULT 14  
US-09-755-.274-29  
; Sequence 29, Application US/09755274  
; Patent No. 6657046  
; GENERAL INFORMATION:

RESULT 15  
 US-09-755-630B-7  
 Sequence 7, Application US/09755630B  
 Patent No. 6639054  
 GENERAL INFORMATION:  
 APPLICANT: ALIBHAI, MURTAZA F.  
 APPLICANT: ALWOOD, JAMES D.  
 APPLICANT: SAMPSON, HUGH A.  
 APPLICANT: McHERTER, CHARLES A.  
 TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMOLEINS  
 FILE REFERENCE: 11899.0217.NPUS00 (MOB1217)  
 CURRENT APPLICATION NUMBER: US/09/755,630B  
 CURRENT FILING DATE: 2001-01-05  
 PRIOR APPLICATION NUMBER: US 60/174,669  
 PRIOR FILING DATE: 2000-01-06  
 NUMBER OF SEQ ID NOS: 295  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 7  
 LENGTH: 367  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic polypeptide  
 US-09-755-630B-7

QY 14 QLGEMTVLSIDGGIRGIIPATILEFLEGQLQEMDNADARLADYFDVIGGTSTGGLT 203



Db	5	QIGEMVTVLSIDGGIRGIIIPATILFLEBQIQEMDNNADARLADYFDVIGTSGGLT	64
Qy	204	AMISTPENENRRPPAAAKEIYPFEHGPQIFNPSGQILGPKYDKYIMQVLQEKLGSTRV	263
Db	65	AMISTPENENRRPPAAAKEIYPFEHGPQIFNPSGQILGPKYDKYIMQVLQEKLGSTRV	124
Qy	264	HOALTEVVISSPDIKTNKPVIFTKSNLANSPELDKMYDISYSTAAAPTYFPHYFVTNT	323
Db	125	HOALTEVVISSPDIKTNKPVIFTKSNLANSPELDKMYDISYSTAAAPTYFPHYFVTNT	184
Qy	324	SNGDEYEENLVGDGAVATVADPALLSISVATRLAQKDPAPASIR	366
Db	185	SNGDEYEENLVGDGAVATVADPALLSISVATRLAQKDPAPASIR	227

Search completed: April 8, 2005, 07:57:52  
 Job time : 43 secs

.....page blank (uspto)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2005, 07:56:20 ; Search time 55 Seconds  
(without alignments)  
2209.291 Million cell updates/sec

Title: US-10-658-180-247

Perfect score: 1865

Sequence: 1 SLNYKKMLLSLTGTTSEF.....LSISVATRLAQKDPAFASIR 366

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 33197259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppaa/PCR\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubppaa/PCRUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubppaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubppaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubppaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubppaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubppaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubppaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubppaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1865	100.0	366	10	US-09-755-630A-247 Sequence 247, App
2	1865	100.0	366	10	US-09-755-630A-271 Sequence 271, App
3	1765	94.9	366	10	US-09-755-630A-275 Sequence 275, App
4	1753	94.0	366	10	US-09-755-630A-259 Sequence 259, App
5	1645	88.2	366	10	US-09-755-630A-251 Sequence 251, App
6	1544	82.8	366	10	US-09-755-630A-255 Sequence 255, App
7	1480	79.4	366	10	US-09-755-630A-263 Sequence 263, App
8	1139	61.1	366	10	US-09-755-630A-7 Sequence 7, App1
9	1139	61.1	366	10	US-09-755-630A-2 Sequence 2, App1
10	1139	61.1	366	10	US-09-755-630A-265 Sequence 265, App
11	1139	61.1	366	10	US-09-755-630A-286 Sequence 286, App
12	1139	61.1	452	10	US-09-755-630A-6 Sequence 6, App1
13	1019	54.6	386	10	US-09-755-630A-279 Sequence 279, App

14	1017	54.5	386	10	US-09-755-630A-278 Sequence 278, App
15	1014	54.4	386	10	US-09-755-630A-282 Sequence 282, App
16	1013	54.3	366	10	US-09-755-630A-281 Sequence 281, App
17	1001.5	53.7	365	10	US-09-755-630A-280 Sequence 280, App
18	618.5	33.2	335	15	US-10-424-599-143308 Sequence 143308, App
19	609.5	32.7	405	16	US-10-437-963-129647 Sequence 129647, App
20	585	31.4	387	16	US-10-437-963-177823 Sequence 177823, App
21	579	31.0	400	14	US-10-150-4298-1 Sequence 1, App1
22	565.5	30.3	438	15	US-10-425-114-72032 Sequence 72032, A
23	565.5	30.3	438	15	US-10-425-114-72035 Sequence 72035, A
24	565.5	30.3	448	15	US-10-425-114-65072 Sequence 65072, A
25	545	29.2	442	16	US-10-437-963-138254 Sequence 138254, App
26	545	29.2	1275	16	US-10-437-963-199835 Sequence 199835, App
27	544.5	29.2	431	16	US-10-437-963-108232 Sequence 108232, App
28	537.5	28.8	430	16	US-10-437-963-109130 Sequence 109130, App
29	534.5	28.7	390	14	US-10-034-937-4 Sequence 4, App1
30	534.5	28.7	390	14	US-10-034-937-10 Sequence 10, App1
31	533	28.6	390	14	US-10-034-937-12 Sequence 12, App1
32	531.5	28.5	390	14	US-10-034-937-38 Sequence 38, App1
33	529.5	28.4	390	14	US-10-034-937-8 Sequence 8, App1
34	528.5	28.3	387	14	US-10-034-937-42 Sequence 42, App1
35	528.5	28.3	390	14	US-10-034-937-16 Sequence 16, App1
36	528.5	28.3	390	14	US-10-034-937-20 Sequence 20, App1
37	528.5	28.3	390	14	US-10-034-937-32 Sequence 32, App1
38	528.5	28.3	390	14	US-10-034-937-34 Sequence 34, App1
39	528.5	28.3	390	14	US-10-034-937-41 Sequence 41, App1
40	528.5	28.3	408	14	US-09-755-630A-287 Sequence 287, App
41	528.5	28.3	477	16	US-10-437-963-137697 Sequence 137697, App
42	528.5	28.3	390	14	US-10-034-937-6 Sequence 6, App1
43	527.5	28.3	386	14	US-10-034-937-2 Sequence 2, App1
44	527	28.3	390	14	US-10-034-937-22 Sequence 22, App1
45	527	28.3	390	14	US-10-034-937-22 Sequence 22, App1

#### ALIGNMENTS

RESULT 1  
US-09-755-630A-247  
Sequence 247, Application US/09755630A  
Publication No. US20030194399A1  
GENERAL INFORMATION:  
APPLICANT: ALTBHAI, MURTAZA F.  
APPLICANT: ASTWOOD, JAMES D.  
APPLICANT: SAMPSON, HUGH A.  
APPLICANT: MCWHERTER, CHARLES A.  
TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMOTELINS  
FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)  
CURRENT APPLICATION NUMBER: US/09/755,630A  
CURRENT FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: US 60/174,669  
PRIOR FILING DATE: 2000-01-06  
NUMBER OF SEQ ID NOS: 293  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 247  
LENGTH: 366  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic polypeptide  
US-09-755-630A-247

Query Match 100.0%; Score 1865; DB 10; Length 366;  
Best Local Similarity 100.0%; Pred. No. 2.7e-157;  
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLNYKKMLLSLTGTTSEFDTYTAKEALTWAVHMLVYQKWTDAASMYDDYVSTA 60  
DB 1 SLNYKKMLLSLTGTTSEFDTYTAKEALTWAVHMLVYQKWTDAASMYDDYVSTA 60  
QY 61 FOALDSKNYLYRVOENALVTGTTTMDASANNELLVQVGENILKKPVSDNPETYEAL 120  
DB 61 FOALDSKNYLYRVOENALVTGTTTMDASANNELLVQVGENILKKPVSDNPETYEAL 120

```

QY      121 KRFPAKLSDRKKLRANKASVGPQLGEMVTVLSDGGIRGIIIPATILEFLGQLOEMDN 180
      121 KRFPAKLSDRKKLRANKASVGPQLGEMVTVLSDGGIRGIIIPATILEFLGQLOEMDN 180
QY      181 NADARLADYDVIGSTGTGLTAMISTPNNRRPFAAKEIVPFYFHEGPQIFNPSGOI 240
      181 NADARLADYDVIGSTGTGLTAMISTPNNRRPFAAKEIVPFYFHEGPQIFNPSGOI 240
Db      181 NADARLADYDVIGSTGTGLTAMISTPNNRRPFAAKEIVPFYFHEGPQIFNPSGOI 240
QY      241 LGRKYDGKYLMOVLQEKLGSTRVHQAALTEVVISSPDIKTNKPVIPTKSNLANSPELDAM 300
      241 LGRKYDGKYLMOVLQEKLGSTRVHQAALTEVVISSPDIKTNKPVIPTKSNLANSPELDAM 300
Db      241 LGRKYDGKYLMOVLQEKLGSTRVHQAALTEVVISSPDIKTNKPVIPTKSNLANSPELDAM 300
QY      301 YDISYSTAAAPTYFPFHYFVTNTSNGDEYFENLVDAVATVADPALLISVATRLAQKDP 360
      301 YDISYSTAAAPTYFPFHYFVTNTSNGDEYFENLVDAVATVADPALLISVATRLAQKDP 360
Db      301 YDISYSTAAAPTYFPFHYFVTNTSNGDEYFENLVDAVATVADPALLISVATRLAQKDP 360
QY      361 AFASIR 366
      361 AFASIR 366
      361 AFASIR 366

```

## RESULT 2

```

US-09-755-630A-271
; Sequence 271, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTEINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755,630A
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 271
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-271

```

Query Match 100.0%; Score 1865; DB 10; Length 389;

Best Local Similarity 100.0%; Pred. No. 2.9e-157; Indels 0; Gaps 0;

Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 SLNYKKLLSLGTTSEFDKTYTAKEATWTAVHMLVIQKMTDAASVMTDYLLSTA 60
      1 SLNYKKLLSLGTTSEFDKTYTAKEATWTAVHMLVIQKMTDAASVMTDYLLSTA 60
Db      24 SLNYKKLLSLGTTSEFDKTYTAKEATWTAVHMLVIQKMTDAASVMTDYLLSTA 83
QY      61 FOALDSKNYLRVQENALJTETEMDASEANMELLVOGSENLKKPVSNDNPEYEEAL 120
      61 FOALDSKNYLRVQENALJTETEMDASEANMELLVOGSENLKKPVSNDNPEYEEAL 120
Db      84 FOALDSKNYLRVQENALJTETEMDASEANMELLVOGSENLKKPVSNDNPEYEEAL 143
QY      121 KRFPAKLSDRKKLRANKASVGPQLGEMVTVLSDGGIRGIIIPATILEFLGQLOEMDN 180
      121 KRFPAKLSDRKKLRANKASVGPQLGEMVTVLSDGGIRGIIIPATILEFLGQLOEMDN 180
Db      144 KRFPAKLSDRKKLRANKASVGPQLGEMVTVLSDGGIRGIIIPATILEFLGQLOEMDN 203
QY      181 NADARLADYDVIGSTGTGLTAMISTPNNRRPFAAKEIVPFYFHEGPQIFNPSGOI 240
      181 NADARLADYDVIGSTGTGLTAMISTPNNRRPFAAKEIVPFYFHEGPQIFNPSGOI 240
Db      204 NADARLADYDVIGSTGTGLTAMISTPNNRRPFAAKEIVPFYFHEGPQIFNPSGOI 263
QY      241 LGRKYDGKYLMOVLQEKLGSTRVHQAALTEVVISSPDIKTNKPVIPTKSNLANSPELDAM 300
      241 LGRKYDGKYLMOVLQEKLGSTRVHQAALTEVVISSPDIKTNKPVIPTKSNLANSPELDAM 300
Db      264 LGRKYDGKYLMOVLQEKLGSTRVHQAALTEVVISSPDIKTNKPVIPTKSNLANSPELDAM 323
QY      301 YDISYSTAAAPTYFPFHYFVTNTSNGDEYFENLVDAVATVADPALLISVATRLAQKDP 360
      301 YDISYSTAAAPTYFPFHYFVTNTSNGDEYFENLVDAVATVADPALLISVATRLAQKDP 360

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Db      324 YDISYSTAAAPTYFPFHYFVTNTSNGDEYFENLVDAVATVADPALLISVATRLAQKDP 383
QY      361 AFASIR 366
      361 AFASIR 366
Db      384 AFASIR 389

```

## RESULT 3

```

US-09-755-630A-275
; Sequence 275, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTEINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755,630A
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 275
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-275

```

Query Match 94.9%; Score 1769; DB 10; Length 389;

Best Local Similarity 96.7%; Pred. No. 1e-148; Indels 8; Gaps 0;

Matches 348; Conservative 4; Mismatches 8; Indels 8; Gaps 0;

```

QY      7 MLNLSLGTGTTSEFDKTYTAKEATWTAVHMLVIQKMTDAASVMTDYLLSTAFOALDS 66
      7 MLNLSLGTGTTSEFDKTYTAKEATWTAVHMLVIQKMTDAASVMTDYLLSTAFOALDS 66
Db      8 LILIFMILATTSSTFAVYTAKEATWTAVHMLVIQKMTDAASVMTDYLLSTAFOALDS 67
QY      67 KNNYLRVQENALJTETEMDASEANMELLVOGSENLKKPVSNDNPEYEEALKRFPAKL 126
      67 KNNYLRVQENALJTETEMDASEANMELLVOGSENLKKPVSNDNPEYEEALKRFPAKL 126
Db      68 KNNYLRVQENALJTETEMDASEANMELLVOGSENLKKPVSNDNPEYEEALKRFPAKL 127
QY      127 LSDRKKLRANKASVGPQLGEMVTVLSDGGIRGIIIPATILEFLGQLOEMDNADARL 186
      127 LSDRKKLRANKASVGPQLGEMVTVLSDGGIRGIIIPATILEFLGQLOEMDNADARL 186
Db      128 LSDRKKLRANKASVGPQLGEMVTVLSDGGIRGIIIPATILEFLGQLOEMDNADARL 187
QY      187 ADVFVYIGSTGTGLTAMISTPNNRRPFAAKEIVPFYFHEGPQIFNPSGOILGPKYD 246
      187 ADVFVYIGSTGTGLTAMISTPNNRRPFAAKEIVPFYFHEGPQIFNPSGOILGPKYD 246
Db      188 ADVFVYIGSTGTGLTAMISTPNNRRPFAAKEIVPFYFHEGPQIFNPSGOILGPKYD 247
QY      247 GKYLMOVLQEKLGSTRVHQAALTEVVISSPDIKTNKPVIPTKSNLANSPELDAMDISYS 306
      247 GKYLMOVLQEKLGSTRVHQAALTEVVISSPDIKTNKPVIPTKSNLANSPELDAMDISYS 306
Db      248 GKYLMOVLQEKLGSTRVHQAALTEVVISSPDIKTNKPVIPTKSNLANSPELDAMDISYS 307
QY      307 TAAAPTYFPFHYFVTNTSNGDEYFENLVDAVATVADPALLISVATRLAQKDPAFASIR 366
      307 TAAAPTYFPFHYFVTNTSNGDEYFENLVDAVATVADPALLISVATRLAQKDPAFASIR 366
Db      308 TAAAPTYFPFHYFVTNTSNGDEYFENLVDAVATVADPALLISVATRLAQKDPAFASIR 367

```

## RESULT 4

```

US-09-755-630A-259
; Sequence 259, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTEINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755,630A

```

;; CURRENT FILING DATE: 2001-01-05  
;; PRIOR APPLICATION NUMBER: US 60/174,669  
;; PRIOR FILING DATE: 2000-01-06  
;; NUMBER OF SEQ ID NOS: 293  
;; SOFTWARE: Patentin version 3.0  
;; SEQ ID NO 259  
;; LENGTH: 366  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic polypeptide  
US-09-755-630A-259

Query Match 94.0%; Score 1753; DB 10; Length 366;  
Best Local Similarity 99.7%; Pred. No. 2,5e-147;  
Matches 343; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 TTTAKAAATWTAVHMLVIOKMTDAASSYMTDYLLSTAFQALDSKNNYLKVOENALTGTT 82  
DB 1 TTTAKAAATWTAVHMLVIOKMTDAASSYMTDYLLSTAFQALDSKNNYLKVOENALTGTT 60  
QY 83 TEMDDASEANMELLVOGENTLKKPVSEDPETYEALKRFALISDRKKLRANKASYCP 142  
DB 61 TEMDDASEANMELLVOGENTLKKPVSEDPETYEALKRFALISDRKKLRANKASYCP 120  
QY 143 GOLGEVNTLSIDGGIRGIIIPATILIEFLEGLOEMDNADRLADYFDVIGTSTGGIL 202  
DB 121 GOLGEVNTLSIDGGIRGIIIPATILIEFLEGLOEMDNADRLADYFDVIGTSTGGIL 180  
QY 203 TAMISTPNNRPPFAAKEIVPFYFEHGPQIFNPSCQILGPXYDGKYLMOVLQEKGETR 262  
DB 181 TAMISTPNNRPPFAAKEIVPFYFEHGPQIFNPSCQILGPXYDGKYLMOVLQEKGETR 240  
QY 263 VHOALTEVVISFDIKTKNPVITTKSNLANSPELDAMVDISYTAAPTYPPPHYFTN 322  
DB 241 VHOALTEVVISFDIKTKNPVITTKSNLANSPELDAMVDISYTAAPTYPPPHYFTN 300  
QY 323 TSNNGDEYEFNLVDGAATVADPALLSISVATRLAODPAPASIR 366  
DB 301 TSNNGDEYEFNLVDGAATVADPALLSISVATRLAODPAPASIR 344

RESULT 5  
US-09-755-630A-251  
;; Sequence 251, Application US/09755630A  
;; Publication No. US20030194399A1  
;; GENERAL INFORMATION:  
;; APPLICANT: ALIBHAI, MURTAZA F.  
;; APPLICANT: ASTWOOD, JAMES D.  
;; APPLICANT: SAMPSON, HUGH A.  
;; APPLICANT: MCMHERTER, CHARLES A.  
;; TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTATEINS  
;; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)  
;; CURRENT APPLICATION NUMBER: US/09/755,630A  
;; CURRENT FILING DATE: 2001-01-05  
;; PRIOR APPLICATION NUMBER: US 60/174,669  
;; PRIOR FILING DATE: 2000-01-06  
;; NUMBER OF SEQ ID NOS: 293  
;; SOFTWARE: Patentin version 3.0  
;; SEQ ID NO 251  
;; LENGTH: 366  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic polypeptide  
US-09-755-630A-251

Query Match 88.2%; Score 1645; DB 10; Length 366;  
Best Local Similarity 100.0%; Pred. No. 1e-137;  
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLNYKKMLLSLGTGTTSEFDKTYTAKAATWTAVHMLVIOKMTDAASSYMTDYLLSTA 60  
|||||

DB 46 SLNYKKMLLSLGTGTTSEFDKTYTAKAATWTAVHMLVIOKMTDAASSYMTDYLLSTA 105  
QY 61 FOALDSKNNYLKVOENALGTTTEMDDASEANMELLVOGENTLKKPVSEDPETYEAL 120  
DB 106 FOALDSKNNYLKVOENALGTTTEMDDASEANMELLVOGENTLKKPVSEDPETYEAL 165  
QY 121 KRPAKLISDRKKLRANKASYGPGQLEGEMTVLISIDGGIRGIIIPATILIEFLEGLOEMDN 180  
DB 166 KRPAKLISDRKKLRANKASYGPGQLEGEMTVLISIDGGIRGIIIPATILIEFLEGLOEMDN 225  
QY 181 NADARLADYFDVIGTSTGGILTAMISTPNNRPPFAAKEIVPFYFEHGPQIFNPSCQI 240  
DB 226 NADARLADYFDVIGTSTGGILTAMISTPNNRPPFAAKEIVPFYFEHGPQIFNPSCQI 285  
QY 241 LGPKYDGKYLMOVLQEKLETRVHQALETEVVISFDIKTKNPVITTKSNLANSPELDAM 300  
DB 286 LGPKYDGKYLMOVLQEKLETRVHQALETEVVISFDIKTKNPVITTKSNLANSPELDAM 345  
QY 301 YDISYSTAAAPTYPPPHYFT 321  
DB 346 YDISYSTAAAPTYPPPHYFT 366

RESULT 6  
US-09-755-630A-255  
;; Sequence 255, Application US/09755630A  
;; Publication No. US20030194399A1  
;; GENERAL INFORMATION:  
;; APPLICANT: ALIBHAI, MURTAZA F.  
;; APPLICANT: ASTWOOD, JAMES D.  
;; APPLICANT: SAMPSON, HUGH A.  
;; APPLICANT: MCMHERTER, CHARLES A.  
;; TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTATEINS  
;; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)  
;; CURRENT APPLICATION NUMBER: US/09/755,630A  
;; CURRENT FILING DATE: 2001-01-05  
;; PRIOR APPLICATION NUMBER: US 60/174,669  
;; PRIOR FILING DATE: 2000-01-06  
;; NUMBER OF SEQ ID NOS: 293  
;; SOFTWARE: Patentin version 3.0  
;; SEQ ID NO 255  
;; LENGTH: 366  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic polypeptide  
US-09-755-630A-255

Query Match 82.8%; Score 1544; DB 10; Length 366;  
Best Local Similarity 100.0%; Pred. No. 1e-128;  
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSLGTGTTSEFDKTYTAKAATWTAVHMLVIOKMTDAASSYMTDYLLSTA 60  
DB 64 SLNYKKMLLSLGTGTTSEFDKTYTAKAATWTAVHMLVIOKMTDAASSYMTDYLLSTA 123  
QY 61 FOALDSKNNYLKVOENALGTTTEMDDASEANMELLVOGENTLKKPVSEDPETYEAL 120  
DB 124 FOALDSKNNYLKVOENALGTTTEMDDASEANMELLVOGENTLKKPVSEDPETYEAL 183  
QY 121 KRPAKLISDRKKLRANKASYGPGQLEGEMTVLISIDGGIRGIIIPATILIEFLEGLOEMDN 180  
DB 184 KRPAKLISDRKKLRANKASYGPGQLEGEMTVLISIDGGIRGIIIPATILIEFLEGLOEMDN 243  
QY 181 NADARLADYFDVIGTSTGGILTAMISTPNNRPPFAAKEIVPFYFEHGPQIFNPSCQI 240  
DB 244 NADARLADYFDVIGTSTGGILTAMISTPNNRPPFAAKEIVPFYFEHGPQIFNPSCQI 303  
QY 241 LGPKYDGKYLMOVLQEKLETRVHQALETEVVISFDIKTKNPVITTKSNLANSPELDAM 300  
DB 304 LGPKYDGKYLMOVLQEKLETRVHQALETEVVISFDIKTKNPVITTKSNLANSPELDAM 363  
QY 301 YDI 303

Db 364 YDI 366

## RESULT 7

US-09-755-630A-263  
Sequence 263, Application US/09755630A  
Publication No. US20030194399A1  
GENERAL INFORMATION:  
APPLICANT: ALIBHAI, MURTAZA F.  
APPLICANT: ASTWOOD, JAMES D.  
APPLICANT: SAMPOON, HUGH A.  
APPLICANT: MCWHERTER, CHARLES A.  
TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTTEINS  
FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)  
CURRENT APPLICATION NUMBER: US/09/755,630A  
CURRENT FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: US 60/174,669  
PRIOR FILING DATE: 2000-01-06  
NUMBER OF SEQ ID NOS: 293  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 263  
LENGTH: 366  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic polypeptide  
US-09-755-630A-263

Query Match 79.4%; Score 1480; DB 10; Length 366;  
Best Local Similarity 100.0%; Pred. No. 5e-123;  
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 76 NATGGTTEMDDBSEANMELLVOYGENLLKKPVSEDPETYEALKKRFAKLSDRKLRA 135  
1 NATGGTTEMDDBSEANMELLVOYGENLLKKPVSEDPETYEALKKRFAKLSDRKLRA 60  
QY 136 NKASYGFGQLEWTVLSIDGGIRGIIIPATILEFLEGQLOEMDNADALADYFDVIGG 195  
Db 61 NKASYGFGQLEWTVLSIDGGIRGIIIPATILEFLEGQLOEMDNADALADYFDVIGG 120  
QY 196 TSTGGILTAMISTPENNRRPFAAKEIVPFYFEGPOIFNPSGQILGPKYDGLMOVLQ 255  
Db 121 TSTGGILTAMISTPENNRRPFAAKEIVPFYFEGPOIFNPSGQILGPKYDGLMOVLQ 180  
QY 256 EKGTEHVHQAITEVVISPDIKNKPVIFTKSNLANSPELDAMVDISYSTAAPTYFP 315  
Db 181 EKGTEHVHQAITEVVISPDIKNKPVIFTKSNLANSPELDAMVDISYSTAAPTYFP 240  
QY 316 PHYFVNTSNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 366  
Db 241 PHYFVNTSNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 291

## RESULT 8

US-09-755-630A-7  
Sequence 7, Application US/09755630A  
Publication No. US20030194399A1  
GENERAL INFORMATION:  
APPLICANT: ALIBHAI, MURTAZA F.  
APPLICANT: ASTWOOD, JAMES D.  
APPLICANT: SAMPOON, HUGH A.  
APPLICANT: MCWHERTER, CHARLES A.  
TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTTEINS  
FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)  
CURRENT APPLICATION NUMBER: US/09/755,630A  
CURRENT FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: US 60/174,669  
PRIOR FILING DATE: 2000-01-06  
NUMBER OF SEQ ID NOS: 293  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 7  
LENGTH: 367

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic polypeptide  
US-09-755-630A-7

Query Match 61.1%; Score 1139; DB 10; Length 367;  
Best Local Similarity 100.0%; Pred. No. 1.1e-92;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 QLEWTVLSIDGGIRGIIIPATILEFLEGQLOEMDNADALADYFDVIGGISTGGLT 203  
Db 5 QLEWTVLSIDGGIRGIIIPATILEFLEGQLOEMDNADALADYFDVIGGISTGGLT 64  
QY 204 AMISTENNRRPFAAKEIVPFYFEGPOIFNPSGQILGPKYDGLMOVLQEKLETRV 263  
Db 65 AMISTENNRRPFAAKEIVPFYFEGPOIFNPSGQILGPKYDGLMOVLQEKLETRV 124  
QY 264 HQALTEVVISPDIKNKPVIFTKSNLANSPELDAMVDISYSTAAPTYFPFHYFVNT 323  
Db 125 HQALTEVVISPDIKNKPVIFTKSNLANSPELDAMVDISYSTAAPTYFPFHYFVNT 184  
QY 324 SNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 366  
Db 185 SNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 227

## RESULT 9

US-09-755-630A-2  
Sequence 2, Application US/09755630A  
Publication No. US20030194399A1  
GENERAL INFORMATION:  
APPLICANT: ALIBHAI, MURTAZA F.  
APPLICANT: ASTWOOD, JAMES D.  
APPLICANT: SAMPOON, HUGH A.  
APPLICANT: MCWHERTER, CHARLES A.  
TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTTEINS  
FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)  
CURRENT APPLICATION NUMBER: US/09/755,630A  
CURRENT FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: US 60/174,669  
PRIOR FILING DATE: 2000-01-06  
NUMBER OF SEQ ID NOS: 293  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 386  
TYPE: PRT  
ORGANISM: Solanum tuberosum  
US-09-755-630A-2

Query Match 61.1%; Score 1139; DB 10; Length 386;  
Best Local Similarity 100.0%; Pred. No. 1.2e-92;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 QLEWTVLSIDGGIRGIIIPATILEFLEGQLOEMDNADALADYFDVIGGISTGGLT 203  
Db 24 QLEWTVLSIDGGIRGIIIPATILEFLEGQLOEMDNADALADYFDVIGGISTGGLT 83  
QY 204 AMISTENNRRPFAAKEIVPFYFEGPOIFNPSGQILGPKYDGLMOVLQEKLETRV 263  
Db 84 AMISTENNRRPFAAKEIVPFYFEGPOIFNPSGQILGPKYDGLMOVLQEKLETRV 143  
QY 264 HQALTEVVISPDIKNKPVIFTKSNLANSPELDAMVDISYSTAAPTYFPFHYFVNT 323  
Db 144 HQALTEVVISPDIKNKPVIFTKSNLANSPELDAMVDISYSTAAPTYFPFHYFVNT 203  
QY 324 SNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 366  
Db 204 SNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 246

## RESULT 10

US-09-755-630A-265

```
; Sequence 265, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTTEINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755.630A
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 265
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-265
```

```
Query Match 61.1%; Score 1139; DB 10; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 144 QLGEMVTVLSDGGIRGIIPATILFELEGQLQEMDNNAARLADYDFVIGTSTGGLT 203
DB 24 QLGEMVTVLSDGGIRGIIPATILFELEGQLQEMDNNAARLADYDFVIGTSTGGLT 83
QY 204 AMISTENNRRPFAAKEIYPFPEHGPQIFNPSGQILGPKYDGKYLMOVLQEKLGSTRV 263
DB 84 AMISTENNRRPFAAKEIYPFPEHGPQIFNPSGQILGPKYDGKYLMOVLQEKLGSTRV 143
QY 264 HQALTEVVISFPDIKTKNPVIFTKSNLANSPELDKAKYDISYTAAPTYFPFHYFTNT 323
DB 144 HQALTEVVISFPDIKTKNPVIFTKSNLANSPELDKAKYDISYTAAPTYFPFHYFTNT 203
QY 324 SNGDEYEFNLVDGAVATVADPALISISVATRLAQKDPAPASIR 366
DB 204 SNGDEYEFNLVDGAVATVADPALISISVATRLAQKDPAPASIR 246
```

```
RESULT 11
US-09-755-630A-286
; Sequence 286, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTTEINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755.630A
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 286
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-755-630A-286
```

```
Query Match 61.1%; Score 1139; DB 10; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 144 QLGEMVTVLSDGGIRGIIPATILFELEGQLQEMDNNAARLADYDFVIGTSTGGLT 203
```

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DB 24 QLGEMVTVLSDGGIRGIIPATILFELEGQLQEMDNNAARLADYDFVIGTSTGGLT 83
QY 204 AMISTENNRRPFAAKEIYPFPEHGPQIFNPSGQILGPKYDGKYLMOVLQEKLGSTRV 263
DB 84 AMISTENNRRPFAAKEIYPFPEHGPQIFNPSGQILGPKYDGKYLMOVLQEKLGSTRV 143
QY 264 HQALTEVVISFPDIKTKNPVIFTKSNLANSPELDKAKYDISYTAAPTYFPFHYFTNT 323
DB 144 HQALTEVVISFPDIKTKNPVIFTKSNLANSPELDKAKYDISYTAAPTYFPFHYFTNT 203
QY 324 SNGDEYEFNLVDGAVATVADPALISISVATRLAQKDPAPASIR 366
DB 204 SNGDEYEFNLVDGAVATVADPALISISVATRLAQKDPAPASIR 246
```

```
RESULT 12
US-09-755-630A-6
; Sequence 6, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTTEINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755.630A
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-6
```

```
Query Match 61.1%; Score 1139; DB 10; Length 452;
Best Local Similarity 100.0%; Pred. No. 1.6e-92;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 144 QLGEMVTVLSDGGIRGIIPATILFELEGQLQEMDNNAARLADYDFVIGTSTGGLT 203
DB 90 QLGEMVTVLSDGGIRGIIPATILFELEGQLQEMDNNAARLADYDFVIGTSTGGLT 149
QY 204 AMISTENNRRPFAAKEIYPFPEHGPQIFNPSGQILGPKYDGKYLMOVLQEKLGSTRV 263
DB 150 AMISTENNRRPFAAKEIYPFPEHGPQIFNPSGQILGPKYDGKYLMOVLQEKLGSTRV 209
QY 264 HQALTEVVISFPDIKTKNPVIFTKSNLANSPELDKAKYDISYTAAPTYFPFHYFTNT 323
DB 210 HQALTEVVISFPDIKTKNPVIFTKSNLANSPELDKAKYDISYTAAPTYFPFHYFTNT 269
QY 324 SNGDEYEFNLVDGAVATVADPALISISVATRLAQKDPAPASIR 366
DB 270 SNGDEYEFNLVDGAVATVADPALISISVATRLAQKDPAPASIR 312
```

```
RESULT 13
US-09-755-630A-279
; Sequence 279, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTTEINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755.630A
```

```

; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 279
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-09-755-630A-279
```

```

Query Match      54.6%; Score 1019; DB 10; Length 386;
Best Local Similarity 88.7%; Pred. No. 6e-82;
Matches 197; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
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```

QY 145 LGEWTVLSIDGGIRGIIIPATILFELEGLOEMNNADARLADYFDVIGSTGGLT 204
DB 25 LGEWTVLSIDGGIRGIIIPATILFELEGLOEMNNADARLADYFDVIGSTGGLT 84
QY 205 MISTENNRRPFAAKEIVPFYFEHGPQIFNPSGQILGPKYDGKYLMOVLQEKLG 264
DB 85 MITTENNRRPFAAKDIVPFYFEHGPQIFNPSGQIFGPMYDGKYLQVLQEKLG 144
QY 265 QALTEVVISFDIKTKNPVIFTKSNLANSPELDARLADYDPTVPPHYFVTNTS 324
DB 145 QALTEVAISSFDIKTKNPVIFTKSNLAKSPELDARLADYDPTVPPHYFVTHTS 204
QY 325 NGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366
DB 205 NGDEYEFNLVDGAVATVADPALISVATRLAQVDPKPAASIK 246
```

RESULT 14  
US-09-755-630A-278

```

; Sequence 278, Application US/09755630A
; Publication No. US2003019439A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMHURTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTINS
; FILE REFERENCE: 11899.0217.NPUS00 (WO/217)
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 278
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-09-755-630A-278
```

```

Query Match      54.5%; Score 1017; DB 10; Length 386;
Best Local Similarity 87.9%; Pred. No. 9e-82;
Matches 196; Conservative 13; Mismatches 14; Indels 0; Gaps 0;
```

```

QY 144 QLGEMTVLSIDGGIRGIIIPATILFELEGLOEMNNADARLADYFDVIGSTGGLT 203
DB 24 KLEEMTVLSIDGGIRGIIIPATILFELEGLOEMNNADARLADYFDVIGSTGGLT 83
QY 204 AMISTENNRRPFAAKEIVPFYFEHGPQIFNPSGQILGPKYDGKYLMOVLQEKLG 263
DB 84 AMITTENNRRPFAAKDIVPFYFEHGPQIFNPSGQILGPMYDGKYLQVLQEKLG 143
QY 264 HQALTEVVISFDIKTKNPVIFTKSNLANSPELDARLADYDPTVPPHYFVTNT 323
DB 144 HQALTEVAISSFDIKTKNPVIFTKSNLAKSPELDARLADYDPTVPPHYFVTHT 203
QY 324 SNDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366
DB 204 SNDEYEFNLVDGAVATVADPALISVATRLAQVDPKPAASIK 246
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DB 204 SNDEYEFNLVDGAVATVADPALISVATRLAQEDPAPASSIK 246

RESULT 15

```

US-09-755-630A-282
; Sequence 282, Application US/09755630A
; Publication No. US2003019439A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMHURTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTINS
; FILE REFERENCE: 11899.0217.NPUS00 (WO/217)
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 282
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-09-755-630A-282
```

```

Query Match      54.4%; Score 1014; DB 10; Length 386;
Best Local Similarity 88.3%; Pred. No. 1.7e-81;
Matches 197; Conservative 12; Mismatches 14; Indels 0; Gaps 0;
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```

QY 144 QLGEMTVLSIDGGIRGIIIPATILFELEGLOEMNNADARLADYFDVIGSTGGLT 203
DB 24 KLEEMTVLSIDGGIRGIIIPATILFELEGLOEMNNADARLADYFDVIGSTGGLT 83
QY 204 AMISTENNRRPFAAKEIVPFYFEHGPQIFNPSGQILGPKYDGKYLMOVLQEKLG 263
DB 84 AMITTENNRRPFAAKDIVPFYFEHGPQIFNPSGQILGPMYDGKYLQVLQEKLG 143
QY 264 HQALTEVVISFDIKTKNPVIFTKSNLANSPELDARLADYDPTVPPHYFVTNT 323
DB 144 HQALTEVAISSFDIKTKNPVIFTKSNLAKSPELDARLADYDPTVPPHYFVTHT 203
QY 324 SNDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366
DB 204 SNDEYEFNLVDGAVATVADPALISVATRLAQEDPAPASSIK 246
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Search completed: April 8, 2005, 08:10:38  
Job time : 56 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 8, 2005, 07:38:59 ; Search time 38 Seconds  
(without alignments)  
631.316 Million cell updates/sec

Title: US-10-658-180-247

Perfect score: 1865

Sequence: 1 SLNKKMLLISGTTSEF.....LSIVATRLAQDPAPASIR 366

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 288363 seqs, 65546468 residues

Total number of hits satisfying chosen parameters: 288363

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA New:\*  
1: /cgn2\_6/prodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/paa/US07\_NEW\_COMB.pep:\*  
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5: /cgn2\_6/prodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/paa/US10\_NEW\_COMB.pep:\*  
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8: /cgn2\_6/prodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1014	54.4	386	US-11-061-894-14	Sequence 14, Appl
2	528.5	28.3	408	US-11-061-894-10	Sequence 10, Appl
3	528.5	28.3	408	US-11-061-894-12	Sequence 12, Appl
4	268.5	14.4	350	PCT-US05-07908-100	Sequence 100, Appl
5	242	13.0	378	PCT-US05-07908-18	Sequence 18, Appl
6	239.5	12.8	387	PCT-US05-07908-66	Sequence 66, Appl
7	234.5	12.6	308	PCT-US05-07908-166	Sequence 166, Appl
8	197	10.6	308	PCT-US05-07908-132	Sequence 132, Appl
9	165	8.8	462	PCT-US05-07908-36	Sequence 36, Appl
10	154	8.3	364	US-60-655-875-130981	Sequence 130981, Appl
11	146.5	7.9	314	US-11-061-233-8	Sequence 8, Appl
12	146.5	7.9	314	US-11-061-894-8	Sequence 8, Appl
13	136.5	7.3	239	US-60-655-875-139557	Sequence 139557, Appl
14	133.5	7.2	258	US-60-655-875-127287	Sequence 127287, Appl
15	113	6.1	444	US-11-045-874-10	Sequence 10, Appl
16	106	5.7	140	US-60-655-875-158378	Sequence 158378, Appl
17	105	5.6	3051	PCT-IB03-06509-3039	Sequence 3039, Appl
18	104	5.6	1682	US-10-450-763-37598	Sequence 37598, Appl
19	104	5.6	1682	US-10-450-763-44026	Sequence 44026, Appl
20	104	5.6	2159	US-10-450-763-44023	Sequence 44023, Appl
21	104	5.6	2503	US-10-450-763-37597	Sequence 37597, Appl
22	104	5.6	2503	US-10-450-763-43913	Sequence 43913, Appl
23	104	5.6	2871	US-10-450-763-37602	Sequence 37602, Appl
24	104	5.6	2871	US-10-450-763-43914	Sequence 43914, Appl
25	104	5.6	2871	US-10-450-763-44024	Sequence 44024, Appl

26	104	5.6	2891	US-10-450-763-37599	Sequence 37599, A
27	104	5.6	2891	US-10-450-763-43915	Sequence 43915, A
28	104	5.6	2891	US-10-450-763-44025	Sequence 44025, A
29	103.5	5.5	399	US-11-027-399-3323	Sequence 3323, Ap
30	103.5	5.5	399	US-11-027-843-3323	Sequence 3323, Ap
31	103.5	5.5	399	US-11-027-878-3323	Sequence 3323, Ap
32	103.5	5.5	399	US-11-028-169-3323	Sequence 3323, Ap
33	103.5	5.5	399	US-11-028-204-3323	Sequence 3323, Ap
34	103.5	5.5	399	US-11-027-877-3323	Sequence 3323, Ap
35	103.5	5.5	399	US-11-027-879-3323	Sequence 3323, Ap
36	103.5	5.5	399	US-11-028-149-3323	Sequence 3323, Ap
37	103.5	5.5	399	US-11-027-802-3323	Sequence 3323, Ap
38	103.5	5.5	399	US-11-027-890-3323	Sequence 3323, Ap
39	103.5	5.5	399	US-11-027-892-3323	Sequence 3323, Ap
40	103.5	5.5	399	US-11-028-099-3323	Sequence 3323, Ap
41	103.5	5.5	399	US-11-028-197-3323	Sequence 3323, Ap
42	103.5	5.5	399	US-11-027-844-3323	Sequence 3323, Ap
43	103.5	5.5	399	US-11-028-050-3323	Sequence 3323, Ap
44	103.5	5.5	399	US-11-028-457-3323	Sequence 3323, Ap
45	103.5	5.5	399	US-11-027-891-3323	Sequence 3323, Ap

#### ALIGNMENTS

```
RESULT 1
US-11-061-894-14
; Sequence 14, Application US/11061894
; GENERAL INFORMATION:
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Abad, Andre R.
; TITLE OF INVENTION: Methods for Enhancing Insect Resistance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 035718/28612
; CURRENT APPLICATION NUMBER: US/11/061,894
; PRIOR FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/546,845
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: 60/546,533
; PRIOR FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-11-061-894-14

Query Match      54.4%; Score 1014; DB 7; Length 386;
Best Local Similarity 88.3%; Pred. No. 9e-76;
Matches 196; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 145 LGMVTVLSIDGGIGIIPATILFELEGLOEMDNADARLADYDVIGTSTGILLTA 204
    |||||
DB 25 LGMVTVLSIDGGIGIIPATILFELEGLOEMDNADARLADYDVIGTSTGILLTA 84
    |||||
QY 205 MISTPENNRPFAAEKEIYPPFHEHGPQIFNPSGQILGPKYDKKTYLMQVLOEKLGRVH 264
    |||||
DB 85 MITTPENNRPFAAADIYFPFHEHGPQIFNPSGQILGPKYDKKTYLMQVLOEKLGRVH 144
    |||||
QY 265 QALTEVVISFDIKTKNPVIFTKSNLANSPELDKAKYDYSYTRAAPTYEPHYPTNTS 324
    |||||
DB 145 QALTEVAISSFDIKTKNPVIFTKSNLANSPELDKAKYDYSYTRAAPTYEPHYPTNTS 204
    |||||
QY 325 NGDEYEFNLVDGAVATVPDALLSISVATRLAQDPAPASIR 366
    |||||
DB 205 NGATYEFNLVDGAVATVPDALLSISVATRLAQDDDAFSSIK 246
    |||||

RESULT 2
US-11-061-894-10
; Sequence 10, Application US/11061894
; GENERAL INFORMATION:
```

```

; APPLICANT: McCutchen, Billy F.
; APPLICANT: Aad, Andre R.
; TITLE OF INVENTION: Methods for Enhancing Insect Resistance
; FILE REFERENCE: 035718/286812
; CURRENT APPLICATION NUMBER: US/11/061,894
; PRIOR FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/546,845
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: 60/546,533
; PRIOR FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Pentaclethra macroloba
US-11-061-894-10
```

```

Query Match      28.3%; Score 528.5; DB 7; Length 408;
Best Local Similarity 53.1%; Pred. No. 1.1e-35;
Matches 113; Conservative 33; Mismatches 50; Indels 17; Gaps 7;
```

```

QY 146 GEMVTVLSIDGGIRGIIPTITLIEFESGLOEMDNNDARLADYFDVIGSTGSLTAM 205
DB 33 GNLVTVLADGGIRGIIIPVILKQLERATLQRMDS--AKLAIEFDVAGTSTGGIITAI 90
QY 206 ISTPNENN--RPPAAKEIVPFYFEHGPQIFNPSGQ-----ILGPKYDGYLMQVLOEKL 258
DB 91 LTPADPQNDKRPPLAAEEIIDFYIEHGPSIFNKSTACSLGIFCPKDKGYLQELISQKL 150
QY 259 GEFTRVQALTEVVISFSDIKTNKPVIFTKSNLANSPELDAMKWDISYSTAAAPTYPPHY 318
DB 151 NETLLDQTTNNVIVPSFDIKLRPTIFSTFKLEVEEVLNKLSDVCMGTSAAPIVPEPPY 210
QY 319 FVTNTSNGDEYEPNLVDGAVATVAD--PALLSIS 350
DB 211 F---KHGDT-EFNLVDGAI--IADIPAPVALS 236
```

## RESULT 3

```

US-11-061-894-12
; Sequence 12, Application US/11061894
; GENERAL INFORMATION:
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Aad, Andre R.
; TITLE OF INVENTION: Methods for Enhancing Insect Resistance
; FILE REFERENCE: 035718/286812
; CURRENT APPLICATION NUMBER: US/11/061,894
; PRIOR FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/546,845
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: 60/546,533
; PRIOR FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Lipase (codon optimized mopentin)
US-11-061-894-12
```

```

Query Match      28.3%; Score 528.5; DB 7; Length 408;
Best Local Similarity 53.1%; Pred. No. 1.1e-35;
Matches 113; Conservative 33; Mismatches 50; Indels 17; Gaps 7;
```

```

QY 146 GEMVTVLSIDGGIRGIIPTITLIEFESGLOEMDNNDARLADYFDVIGSTGSLTAM 205
DB 33 GNLVTVLADGGIRGIIIPVILKQLERATLQRMDS--AKLAIEFDVAGTSTGGIITAI 90
```

```

QY 206 ISTPNENN--RPPAAKEIVPFYFEHGPQIFNPSGQ-----ILGPKYDGYLMQVLOEKL 258
DB 91 LTPADPQNDKRPPLAAEEIIDFYIEHGPSIFNKSTACSLGIFCPKDKGYLQELISQKL 150
QY 259 GEFTRVQALTEVVISFSDIKTNKPVIFTKSNLANSPELDAMKWDISYSTAAAPTYPPHY 318
DB 151 NETLLDQTTNNVIVPSFDIKLRPTIFSTFKLEVEEVLNKLSDVCMGTSAAPIVPEPPY 210
QY 319 FVTNTSNGDEYEPNLVDGAVATVAD--PALLSIS 350
DB 211 F---KHGDT-EFNLVDGAI--IADIPAPVALS 236
```

## RESULT 4

```

PCT-US05-07908-100
; Sequence 100, Application PC/TUS0507908
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: GRAMATIKOVA, Svetlana
; APPLICANT: HAZLEWOOD, Geoff
; APPLICANT: BARTON, Nelson
; APPLICANT: LAM, David
; TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 56446-20042.49
; CURRENT APPLICATION NUMBER: PCT/US05/07908
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: 10/796,907
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: 10/421,654
; PRIOR FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 60/374,313
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample.
PCT-US05-07908-100
```

```

Query Match      14.4%; Score 268.5; DB 1; Length 350;
Best Local Similarity 34.1%; Pred. No. 2.6e-14;
Matches 74; Conservative 45; Mismatches 73; Indels 25; Gaps 8;
```

```

QY 151 VLSIDGGIRGIIPTITLIEFESGLOEMDNNDARLADYFDVIGSTGSLTAMISTPN 210
DB 6 ILISIDGGIRGIIIPALIVELAKRLGLP-----LHKAFDMAGTSTGGIITAGLCFPH 59
QY 211 ENNRPPAAA--KEIVPFYFEHGPQIF-----NPSGQILGPKYDGYLMQVLOEKL 259
DB 60 PDDEETRACTPDLKLYVDHGGKIFENKPIILGNLIPFG--LNDPRQPPDELEKRLAAQIG 118
QY 260 ET-RVHQALTEVVISFSDIKTNKPVIFTKSNLANSPELDAMKWDISYSTAAAPTYPPHY 318
DB 119 LFTATLDKGLTKVILITAYDIQRLQALFMANTDMENS---NFRVYEAARATSAAPTYPPAL 175
QY 319 FV-TNTSNGDEYEPNLVDGAVATVADPALLSISVATR 354
DB 176 IERVGRKNDKRPVPLIDGV--FANDPILAAVYEAR 210
```

## RESULT 5

```

PCT-US05-07908-18
; Sequence 18, Application PC/TUS0507908
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: GRAMATIKOVA, Svetlana
; APPLICANT: HAZLEWOOD, Geoff
; APPLICANT: BARTON, Nelson
; APPLICANT: LAM, David
```

;; TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM  
;; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM  
;; FILE REFERENCE: 56446-20042.49  
;; CURRENT APPLICATION NUMBER: PCT/US05/07908  
;; CURRENT FILING DATE: 2005-03-08  
;; PRIOR APPLICATION NUMBER: 10/796,907  
;; PRIOR FILING DATE: 2004-03-08  
;; PRIOR APPLICATION NUMBER: 10/421,654  
;; PRIOR FILING DATE: 2003-04-21  
;; PRIOR APPLICATION NUMBER: 60/374,313  
;; PRIOR FILING DATE: 2002-04-19  
;; NUMBER OF SEQ ID NOS: 174  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 18  
;; LENGTH: 378  
;; TYPE: PRT  
;; ORGANISM: Unknown  
;; FEATURE:  
;; OTHER INFORMATION: Obtained from an environmental sample.  
PCT-US05-07908-18

Query Match 13.0%; Score 242; DB 1; Length 378;  
Best Local Similarity 29.6%; Pred. No. 4,4e-12;  
Matches 72; Conservative 37; Mismatches 96; Indels 38; Gaps 7;

QY 130 RKGLRANKASYGPGQLEGEMTVLSTIDGGIRGIIPATILEFLLEGQLOEMDNADARLADY 189  
DB 2 KSLQOHLADGSPK-----NILSLDGGIRGALTGLFKLKSIIQE-RHGKDYLLCDH 55  
QY 190 FDIYIGSTSGTLTAMISTPENNRPFAAKEIVPFYFEGHPOIFNPSGQILGPKYDGKY 249  
DB 56 FDIIGSTSGITIAALALIG-----MYVEITIKMTMDLGKIFGKGRSFMRPWETAKY 108  
QY 250 LMQVLOEKLGTEVHQALTEVVISPDIKTNKPVIFTKS-----LANSPELDKMYDI 303  
DB 109 LKAGYHKLKSLKAFQFLGSDIRGLCTIVAKRADTNSIWPILINPK--GKEYDS 166  
QY 304 SY-----STAAPYFPFYPYFNTNSNGEYFNLVDAVAIVADPALLSIS 350  
DB 167 EGGKNNIPLMVAVRASTAAPTYFAPOLI---DVGGQRAAFVGGVSMANNPALTLLK 222  
QY 351 VAT 353  
DB 223 VAT 225

RESULT 6  
PCT-US05-07908-66  
;; Sequence 66, Application PC/TUS0507908  
;; GENERAL INFORMATION:  
;; APPLICANT: DIVERSA CORPORATION  
;; APPLICANT: GRAMATIKOVA, Svetlana  
;; APPLICANT: HAZLEWOOD, Geoff  
;; APPLICANT: BARTON, Nelson  
;; APPLICANT: LAM, David  
;; TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM  
;; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM  
;; FILE REFERENCE: 56446-20042.49  
;; CURRENT APPLICATION NUMBER: PCT/US05/07908  
;; CURRENT FILING DATE: 2005-03-08  
;; PRIOR APPLICATION NUMBER: 10/796,907  
;; PRIOR FILING DATE: 2004-03-08  
;; PRIOR APPLICATION NUMBER: 10/421,654  
;; PRIOR FILING DATE: 2003-04-21  
;; PRIOR APPLICATION NUMBER: 60/374,313  
;; PRIOR FILING DATE: 2002-04-19  
;; NUMBER OF SEQ ID NOS: 174  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 66  
;; LENGTH: 387  
;; TYPE: PRT  
;; ORGANISM: Unknown  
;; FEATURE:

;; OTHER INFORMATION: Obtained from an environmental sample.  
PCT-US05-07908-66

Query Match 12.8%; Score 239.5; DB 1; Length 387;  
Best Local Similarity 29.0%; Pred. No. 7,4e-11;  
Matches 73; Conservative 46; Mismatches 82; Indels 51; Gaps 9;

QY 127 LSPRKLANKASYGPGQLEGEMTVLSTIDGGIRGIIPATILEFLLEGQLO-EMDNADAR 185  
DB 5 LBDKIR-----SSGRK-----ILACDGGIGLMSVEILLAKIADLRTRKQXQNFV 52  
QY 186 LADYFDVIGSTSGTLTAMISTPENNRPFAAKEIVPFYFEGHPOIFNPSGQI--LGP 243  
DB 53 LADYFDVIGSTSGITIAALALIG-----MSMAKIRQFYLDGSKQMPDKASLRLQY 105  
QY 244 KYDGKYLMOVLQ-----EKGTEVHQALTEVVISPDIKTNKPVIFTKS-----LANS 253  
DB 106 SYDDEPLARQLRAFPDQLE-----TDAKLSAHLTKTLMMVRNHSSTDS PWPVSNV 158  
QY 294 P-----ELDAKQYDISYSTAAAPTYFPFYPYFNTNSNGEYFNLVDAVATV 341  
DB 159 PVAKYNNIARKDCNLMPLMQLVRASTAAPTYFPFYPYFNTNSNGEYFNLVDAVATV 218  
QY 342 ADPALLSISVAT 353  
DB 219 NNPAVLAFLMAT 230

RESULT 7  
PCT-US05-07908-166  
;; Sequence 166, Application PC/TUS0507908  
;; GENERAL INFORMATION:  
;; APPLICANT: DIVERSA CORPORATION  
;; APPLICANT: GRAMATIKOVA, Svetlana  
;; APPLICANT: HAZLEWOOD, Geoff  
;; APPLICANT: BARTON, Nelson  
;; APPLICANT: LAM, David  
;; TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM  
;; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM  
;; FILE REFERENCE: 56446-20042.49  
;; CURRENT APPLICATION NUMBER: PCT/US05/07908  
;; CURRENT FILING DATE: 2005-03-08  
;; PRIOR APPLICATION NUMBER: 10/796,907  
;; PRIOR FILING DATE: 2004-03-08  
;; PRIOR APPLICATION NUMBER: 10/421,654  
;; PRIOR FILING DATE: 2003-04-21  
;; PRIOR APPLICATION NUMBER: 60/374,313  
;; PRIOR FILING DATE: 2002-04-19  
;; NUMBER OF SEQ ID NOS: 174  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 166  
;; LENGTH: 308  
;; TYPE: PRT  
;; ORGANISM: Unknown  
;; FEATURE:  
;; OTHER INFORMATION: Obtained from environmental sample  
;; NAME/KEY: DOMAIN  
;; LOCATION: (7) ... (191)  
;; OTHER INFORMATION: Patatin-like phospholipase  
PCT-US05-07908-166

Query Match 12.6%; Score 234.5; DB 1; Length 308;  
Best Local Similarity 31.5%; Pred. No. 1,4e-11;  
Matches 75; Conservative 33; Mismatches 75; Indels 55; Gaps 10;

QY 151 VLSIDGGIRGIIPATILEFLLEGQLOEMDNADARLADYFDVIGSTSGTLTAMISTPN 210  
DB 6 ILSIDGGIRGLSALILBERLEAARNW-----LSQVDLIAGSTGIIA----- 50  
QY 211 ENNRPPFAAKEIYP-----FYFEGHPOIFNPS-----GQLGPKYDGKYLMOVLQEK 257  
DB 51 -----LGLAKLSPTQLRNLYQLRGAALPDDSWMDVLDIGKISGADYDKQLTKELKTI 105



OTHER INFORMATION: =80%, HitCoverage=37%, E-value=3e-36, Identity=36%, Hit description: OTHER INFORMATION: =similar to CG6718-PB [Apis mellifera]  
US-60-655-875-130981

Query Match 8.3%; Score 154; DB 8; Length 364;  
Best Local Similarity 27.7%; Pred. No. 7.7e-05;  
Matches 74; Conservative 37; Mismatches 92; Indels 64; Gaps 14;

73 VOENALGGTTTMDASEANMELLVOGENLTKKPSVSDNPEYEEAL-KRPAALLSDRK 131  
24 VLEKKTGTSE-----ESTVKKPECCD---VEEAIWEMQOM---AL 60  
132 KLRANKASYPGQUGENVTVLSDGGIRGIIIPATILEFEGQLOEMDNADRLADY-- 189  
61 KTRRNKQKTPBRKGTGVRALSLDGGIRGVLYVQMLIEMSLAWGEGLAQGHKKPVQ 120  
190 --FDVIGTSTGGLT-AMISTPENNRPFAAKEIVPFYFHHGQILFNSGQILGPKYD 246  
121 KNFMWIIIGTSTGVALVALVSG-----ISLIDALRYLRLDVSFGARAQLIG--YN 170  
247 GKXLMQVLOEKLGFTVHQAALTEVVISFDIKTKKPIFTKSN-LANSPELDACW----- 300  
171 AQNLTFFLQAFGE--NKKMAE--LSRGNIKGLIKGLFTATYVQKPPRLVFRNPFIS 225  
301 -----YD-----ISYTAAPTYF 314  
226 ALNEYDPYKTNIMWLAARYST-AAPTYF 251

## RESULT 11

US-11-061-233-8  
Sequence 8, Application US/11061233  
GENERAL INFORMATION:  
APPLICANT: McCutchen, Billy F.  
APPLICANT: Abad, Andre R.  
APPLICANT: Wong, James F.  
APPLICANT: Yu, Guo Cao  
TITLE OF INVENTION: Lipases and Methods of Use  
FILE REFERENCE: 035718/286811  
CURRENT APPLICATION NUMBER: US/11/061,233  
CURRENT FILING DATE: 2005-02-18  
PRIOR APPLICATION NUMBER: 60/546,605  
PRIOR FILING DATE: 2004-02-20  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 314  
TYPE: PRT  
ORGANISM: Nitrosomonas europaea  
US-11-061-233-8

Query Match 7.9%; Score 146.5; DB 7; Length 314;  
Best Local Similarity 24.3%; Pred. No. 0.00026;  
Matches 55; Conservative 46; Mismatches 92; Indels 33; Gaps 10;

142 PGQUGENVTVLSDGGIRGIIIPATILEFEGQLOEMDNADRLADYFDVIGTSTGGL 201  
7 PG-ASALLRVLTLDGGAKGP-----YTLGVKKEIEAWVGCPLHOKFDFVFTSTGAI 58  
202 LTMISTPENNRPFAAKEIVPFYFHHGQILFNSGQILGPKYDKYLMQVLOEKLG 261  
59 IASILALGH-----SVDSLIELYRKHVFTWS--QKRAPA-RSQALKKLAEVSGDA 107  
262 RVHQAALTEVVISFDIKTKKPIFTKSNLANS-----PELDARWYDISYSTAAPTY 313  
108 TFSQVKTGIGIVTAKWTERPMIF-KGSVAQAHGQVGFVPGSVIADAVKASCSAYPF 166  
314 PPHHYFTNTSNGDEVEFNVLDGAVATVADPALLSISVARRLAKD 359  
167 F--ERTVRTSMGEDI--LIDGGYC-ANNPTLYALADAVOALRSD 207

## RESULT 12

US-11-061-894-8  
Sequence 8, Application US/11061894  
GENERAL INFORMATION:

APPLICANT: McCutchen, Billy F.  
APPLICANT: Abad, Andre R.  
TITLE OF INVENTION: Methods for Enhancing Insect Resistance  
FILE REFERENCE: 035718/286812  
CURRENT APPLICATION NUMBER: US/11/061,894  
CURRENT FILING DATE: 2005-02-18  
PRIOR APPLICATION NUMBER: 60/546,845  
PRIOR FILING DATE: 2004-02-23  
PRIOR APPLICATION NUMBER: 60/546,533  
PRIOR FILING DATE: 2004-02-20  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 314  
TYPE: PRT  
ORGANISM: Nitrosomonas europaea  
US-11-061-894-8

Query Match 7.9%; Score 146.5; DB 7; Length 314;  
Best Local Similarity 24.3%; Pred. No. 0.00026;  
Matches 55; Conservative 46; Mismatches 92; Indels 33; Gaps 10;

142 PGQUGENVTVLSDGGIRGIIIPATILEFEGQLOEMDNADRLADYFDVIGTSTGGL 201  
7 PG-ASALLRVLTLDGGAKGP-----YTLGVKKEIEAWVGCPLHOKFDFVFTSTGAI 58  
202 LTMISTPENNRPFAAKEIVPFYFHHGQILFNSGQILGPKYDKYLMQVLOEKLG 261  
59 IASILALGH-----SVDSLIELYRKHVFTWS--QKRAPA-RSQALKKLAEVSGDA 107  
262 RVHQAALTEVVISFDIKTKKPIFTKSNLANS-----PELDARWYDISYSTAAPTY 313  
108 TFSQVKTGIGIVTAKWTERPMIF-KGSVAQAHGQVGFVPGSVIADAVKASCSAYPF 166  
314 PPHHYFTNTSNGDEVEFNVLDGAVATVADPALLSISVARRLAKD 359  
167 F--ERTVRTSMGEDI--LIDGGYC-ANNPTLYALADAVOALRSD 207

## RESULT 13

US-60-655-875-139557  
Sequence 139557, Application US/60655875  
GENERAL INFORMATION:

APPLICANT: Boukharov, Andrey  
APPLICANT: Du, Zijing  
APPLICANT: Guo, Liang  
APPLICANT: Kovalic, David  
APPLICANT: Lu, Maolong  
APPLICANT: McCarter, James  
APPLICANT: Miller, Nancy  
APPLICANT: Williams, Deryck  
APPLICANT: Vaudin, Mark  
TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS  
FILE REFERENCE: 38-21(53885)  
CURRENT APPLICATION NUMBER: US/60/655,875  
CURRENT FILING DATE: 2005-02-24  
NUMBER OF SEQ ID NOS: 171306  
SEQ ID NO 139557  
LENGTH: 239  
TYPE: PRT  
ORGANISM: Heterodera glycines

OTHER INFORMATION: Coding regions on vcdna: vcdna-SeqID 65980; Strand++; Position=1  
OTHER INFORMATION: -78,643-849,1362-1475,1684-1826,2183-2358  
FEATURE:  
OTHER INFORMATION: Homolog annotation: Hit\_ID=XP\_394049.1; Match level="QueryCoverage  
OTHER INFORMATION: =68%, HitCoverage=21%, E-value=4e-20, Identity=35%", Hit description:

```

OTHER INFORMATION: =similar to CG6718-PB [Apis mellifera]
US-60-655-139557

Query Match      7.3%; Score 136.5; DB 8; Length 239;
Best Local Similarity 25.3%; Pred. No. 0.0012;
Matches 64; Conservative 37; Mismatches 95; Indels 57; Gaps 10;

QY 73 VQENALGTTTMDADASRANMELLVQGENLTKKPVSDNPETFEAL-KRFATLSDRK 131
DB 24 VLEKTKGTGSE-----ESTVKKPECYD---VEEAIWKEMQM--AL 60

QY 132 KLRANKASYGPGQLGEMVTVLSDGGIRGIIPATLLEFLEGQLOEMDNADRLADY-- 189
DB 61 KTRNEGRKTRRRMGVGRALSDGGIRGLVLVQMLIEMESLWYGBGLAQGHEKNPVQ 120

QY 190 --FDVIGTSTGGILT-AMISTPENNNPFAAKEIVFYFHEHPQIFNPSGQILGPKYD 246
DB 121 KNFMWIIGTSTGAIVALALVSG-----TSLDALRLYLRLKDSYFGARQLIG--YN 170

QY 247 GKYLMOVLQELGELGRHQALTEVVISFQDKTKKPVLYFK-----SNLANSPELDKMY 301
DB 171 AQNIETFLQADLFTTATYVG-----QKPELVKFRNFTSDLNEYNDYKTNIW 217

QY 302 DISYSTAAPTYF 314
DB 218 LAARYSSAPTYF 230

RESULT 14
US-60-655-127287
Sequence 127287, Application US/60655875
GENERAL INFORMATION:
APPLICANT: Boukharov, Andrey
APPLICANT: Du, Zhijiang
APPLICANT: Guo, Liang
APPLICANT: Kovalic, David
APPLICANT: Lu, Maolong
APPLICANT: McCarter, James
APPLICANT: Miller, Nancy
APPLICANT: Williams, Deryck
APPLICANT: Vaudin, Mark
APPLICANT: Wu, Wei
TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
FILE REFERENCE: 38-21(53885)
CURRENT APPLICATION NUMBER: US/60/655, 875
CURRENT FILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
SEQ ID NO 127287
LENGTH: 258
TYPE: PRT
ORGANISM: Heterodera glycines
FEATURE:
OTHER INFORMATION: Coding regions on vCDNA: vCDNA=SeqID 53710; Strand=-; Position=1
OTHER INFORMATION: 129,619-750,1035-1159,1403-1560,1608-1656,1896-1929,1992-2066,21
OTHER INFORMATION: -2186
FEATURE:
OTHER INFORMATION: Homolog annotation: Hit ID=NP_872170.1; Match level="QueryCoverage
OTHER INFORMATION: =91%, HitCoverage=24%, E-value=6e-57, Identity=45%", Hit descrip=
OTHER INFORMATION: ankryn and patatin family member (5V188) [Caenorhabditis elegans]
OTHER INFORMATION: emb|CAD54162.1| Hypothetical protein W
US-60-655-127287

Query Match      7.2%; Score 133.5; DB 8; Length 258;
Best Local Similarity 24.0%; Pred. No. 0.0023;
Matches 56; Conservative 39; Mismatches 59; Indels 79; Gaps 12;

QY 114 EYEBALRKFAKLSDRRKKLRANKASYGPGQLGEMVTVLSDGGIRGIIPATLLEFLEG 173
DB 1 DIYDEVLDKLEVSDE-----DTPEDH--NFINVLSDDGGIRGLVLIQILCYER 50

174 QLOEMDNADRLADYFDVIGTSTGGILT--AMISTPENNNPFAAKEIVFYFHE-- 228

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Db      51  IMCG-----PIPPYEDMWGSGTSGAMVTAGLMOGTLHQILQRLYLRFKDMV---FDNR 100
Qy      229 --HBPQIFNBSGQILGPKRYDGKLYLMQVLOEQLGSTRHQALTEVWISSFDIKTKNPVET 286
Db      101  RPHNTQV-----LEKTRQEMG-----AETWFS--DLKMPR-LMFT 133
Qy      287  KSNLA-----NSPELDKMYDISYST-----AAAPTYF 314
Db      134  TTRAEFPVQELMRNRYKLPINDENESELGRTDDDLMLKVLRRSSAAPTYF 186

RESULT 15
US-11-045-874-10
; Sequence 10, Application US/11045874
; GENERAL INFORMATION:
; APPLICANT: Georgia Tech Research Corporation
; TITLE OF INVENTION: Methods and Compositions for NMD (P) (H) Oxidases
; FILE REFERENCE: GTRC130PCT
; CURRENT APPLICATION NUMBER: US/11/045, 874
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: PCT/US03/24067
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 60/399, 850
; PRIOR FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-045-874-10

Query Match          6.1%; Score 113; DB 7; Length 444;
Best Local Similarity 21.0%; Pred. No. 0.25;
Matches 100; Conservative 53; Mismatches 113; Indels 210; Gaps 25;

Qy      4  YKKMLLSLGT-----GTSSEPKTYTAKKAATVAVHMLVIOKM 44
Db      32  YEKINIVISFCGCLPYFVGFPFDPNPTMISRTQEEFEKTGIS----- 73
Qy      45  TDAASSVWTDVYLSSTAQAL--DSKNNYLRYQENALGTTGEMDASEANMELLVOYGEN 102
Db      74  -----VKTNEHALRVDAKNNT-VYKQKGTI-----FNNVTQDLMTATGAK 115
Qy      103  LKKPVEDNDEPYEALKRPF-----AKLISDRKKLRANKASYGPGQLG----- 146
Db      116  PIIPINNINLEN-HYTKNLEDQOKIKGLMDREIK-NIALIGGYIGIEMVEAKNKR 173
Qy      147  -----EMVTVLSID-----GGGI----- 159
Db      174  KNVRLIQDKHILIDSPDEEIVITIMEBELTKYGVNLHTNEFVKSIGEKKAGVVTNNT 233
Qy      160  -----RGITPATIELEEGLOEDMNNADARLADYFPVIGSTGGLLA----- 204
Db      234  YQADAVILATGIKPDV--EFLLENQKTTKNGA-IIVNEY-----DETSIKNIFSAGDCATI 286
Qy      205  --MISTPENNRPPAAAKEIVPFYFEHQPOLFNPFGOLGPKYQGVKLYLMVLOEQLGSTR 262
Db      287  YNIVSKKNE-YIPLATTA-----NLGRIYGENLNGN----- 317
Qy      263  VHQALTEVWISSFDIKTKNPVIFTKSNLANSPELDKMYDISYSTAAAPTYFPPHYEV- 320
Db      318  -HTAF-KOTIGASAIK-----ILSLEAARTGLTEKDAKRLQIKYKT-----IFVKD 361
Qy      321  ---TNTSNGD-----YEFN--LVDCAVATVADPAL-----LSISVATRLAQKD 359
Db      362  KNHTNYVPGQEDLYIKLIYEENTKTIIGQAQYTGKNGAVMRIMHALSTALYSKLTKE 417

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